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From: Sent: To:

Subject:

Li, Ruixiang Tuesday, April 16, 2002 4:13 PM STIC-Biotech/ChemLib Sequence search of Application NO: 09/758,593

Please do a standard search of SEQ ID NOs: 1 and 2 against both the commercial and interference nucleic acid databases.

Thank you very much!

Ruixiang Li GAU 1646 CM1 10E18 Mail Box 10C01 306-0282

**Point of Contact: Toby Port** Technical Info. Specialist CM1 6A04 703-308-3534

SEQ ID NO. 1 329 09

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TYPE OF SEARCH:	
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Litigation:	
Full text:	
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VENDOR/COST(where applic.) STN:
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Medicine; Nishimachi
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Direct Submission
Submitted (23-MAR-2001) Masatsugu Moriyama,
Department of Molecular Biology, Faculty of
86, Yonago, Tottori 683-8503, Japan
(E-mail:moriyama@grape.med.tottori-u.ac.jp,
Fax:81-859-34-8274)
                                                                                                              carcinoma"
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11. 1012
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Best Local Similarity 99.9
Matches 1150; Conservative
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Submitted (18-DEC-2000) Pallavicini A., Biologia, Universita
Padova, via Ugo Bassi 58/b, 35100, ITALY
Location/Qualifiers
1. 1159
                                                                              Homo sapiens

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleo

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleo

Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

1 (Dass 1 to 1159)

Pallavicini,A., Kojic,S., Bean,C., Vainzof,M., Salamon,M.,

Ievolella,C., Bortoletto,G., Pacchioni,B., Trevisan,S.,

Faulkner,G., Lanfranchi,G. and Valle,G.

Characterization of human skeletal muscle Ankrd2
                                          gaggtggtgaaacttctgcaaagccatggagcagacaccaatgtgagggataagctgctg
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ANKRD2 gene; skeletal muscle ankyrin protein
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Sassob, D. A., Galdspink, G. and Coulton, G.R., Moss, J., Yang, S.Y., Gassob, D.A., Goldspink, G. and Coulton, G.R., Sassob, D.A., Geldspink, G. and Coulton, G.R., Geldspink, G. and Coulton, G.R., Geldspink, G. and Coulton, G.R., Geldspink, G. and 
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Location/Qualifiers
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skeletal muscle and cardiac protein.
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Q9erd4 rattus norv Q9eg6 rattus norv Q9zq79 arabidopsis Q9142 homo sapien Q13768 homo sapien Q99407 homo sapien

024241 drosophila

Q9ncp8 drosophila Q9jjp7 mus musculu Q9vsa2 drosophila 99vsa2 drosophila Q61302 mus musculu P97582 rattus norv

O9npl9 homo sapien O9xz37 drosophila

Sequence:

Title:

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Q9SYK5
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O95271 homo sapien
O9n043 macaca fasc
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                GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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Q9NQC9
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Database

O940p3 drosophila O940d8 mus musculu Q61307 mus musculu Q12055 homo sapien Q91974 gallus gall Q9vau5 drosophila Q9vvv3 drosophila Q9vvv3 drosophila Q13484 homo sapien

Ogauwo oryza sativ Ogsyk5 arabidopsis Ogbsk4 homo sapien

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61 QERVRKTSLDLRREIIDVGGIQNLIELRKKRKQKKRDALAASHEPPPEPEEITGPVDEET 120
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Pallavicini A., Kojic S., Bean C., Vainzof M., Salamon M.,
Ievolella C., Bortoletto G., Pacchioni B., Trevisan S., Faulkner G.,
Lanfranchi G., Valle G.;
"Characterization of human skeletal muscle Ankrd2.";
Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ304805; CAC19412.1;
EMBL; AJ304804; CAC19411.1;
                                                                     01-WAR-2001 (TIEMBLIEL 16, Last sequence update)
01-JUN-2001 (TIEMBLIEL 17, Last annotation update)
SKELETAL MUSCLE ANKYRIN PROTEIN 2 (SKELETAL MUSCLE ANKYRIN REPEAT).
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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PROSITE; PS50088; ANK_REPEAT; 4.
PROSITE; PS50297; ANK_REP_REGION; 1.
SEQUENCE 333 AA; 37151 MW; 679736F0491467A8 CRC64;
333 AA
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Best Local Similarity 100.
Matches 329; Conservative
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091qp7 arabidopsis 09h2k2 homo sapien

homo sapien 09h0i4 homo sapien

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 FLKAAVEGKMKVIEKFLADGGSADTCDQFRRTALHRASLEGHMEILEKLLDNGATVDFQD 180
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"Characterization of a member of a new family proteins with ankyrin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-VARIOUS STRAINS; TISSUE-SPLEEN, AND SKELETAL MUSCLE; MEDLINE-20134618; PubMed-10873377; Kemp T.J., Sadusky T.J., Salusky T.J., Salusky T.J., Salusky T.J., Sassoon D.A., Goldspink G., Coulton G.R.; Identification of Ankrd2, a novel skeletal muscle gene coding for stretch-responsive ankyrin-repeat protein."; EmBL; AJ011118; CAB46646.1; \overrightarrow{D} = \cancel{b} | I_1 | I_2 \rangle EmBL; AJ011118; CAB99432.1; HSSP; P25963; LIKN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MEDSEAVQRATALIEQRLAQEEENEKLRGDTRQKLPMDLLVLEDEKHHGAQSAALQKVKG
                 245 EINARDREGDTALHDAVRLNRYKIIKLLLLHGADWATKNLAGKTPTDLVQLWQADTRHAL
                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                            RLDCTAMHWACRGGHLEVVKLLQSHGADTNVRDKLLSTPLHVAVRTGQVEIVEHFLSLGL
                                                                            Length 328;
                                                                                                                                                                                                                                                                                                                                         Last sequence update)
Last annotation update)
PROTEIN (ANKYRIN REPEAT DOMAIN 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           87.7%; Score 1484.5; DB 11; Leus-
on 8%; Pred. No. 7.1e-95;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (SEP-1998) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PS50088; ANK_REPEAT; 4.
PROSITE; PS50297; ANK_REP_REGION; 1.
SEQUENCE 328 AA; 36707 MW; DB90D955EE9D175E CRC64;
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                                                                                                                                                                                 Created)
                                                                                                                                                                                                                                                                                              PRT;
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O9WV06;
O1-NOV-1999 (TrEMBLrel: 12, La
O1-NOV-1999 (TrEMBLrel: 17, La
O1-:UN-2001 (TrEMBLrel: 17, La
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MGD; MGI:1861447; Ankrd2.
InterPro; IPR002110; ANK.
Pfam; PF00023; ank; 4.
SMART; SM00248; ANK; 4.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID-10090;
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121
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SEQUENCE FROM N.A. WEDLING-20011295; PubMed-10542334; WEDLINE-20011295; PubMed-10542334; Aihara Y., Kurabayashi M., Arai M., Kedes L., Nagai R.; Molecular clontog of rabbit CARP CDNA and its regulated expression in adriamycin cardlowyogathy.
                                                                                                                                                           247
65 RKTSLDLRREIIDVGGIQNLIELRKKRKQKKRDALAASHEPPPFEPEFITGPVDEETFLKA 124
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18 GETGEFLP-----DDFRDGQYEAAVTSEKQEQLKTLPAHHVSLAEQQWEREKQLEAEL 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         125 AVEGKMKVIEKFLADGGSADTCDQFRRTALHRASLEGHMEINEKLLDNGATVDFQDRLDC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TAMHWACRGGHLEVVKLLQSHGADTNVRDKLLSTPLHVAVRTGQVEIVEHFLSLGLEINA
                                                                                           Oryctolagus cuniculus (Rabbit).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Lagomorpha, Leporidae, Oryctolagus.
                                                                     RLDCTAMHWACRGGHLEVVKLLQSHGADTNVRDKLUSTPLHVAVRTGQVEIVEHFLSLGL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 319;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS50068; ANK_REPKAT; 4.
PROSITE; PS50297; ANK_REP_REGION; 1.
SEGUENCE 319 AA; 36245 MN; C7EF87A02936FED3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DI-MAY-2000 (TrEMBLrel. 13, Created)
N-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DI-JUN-2001 (TrEMBLrel. 17, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             40.0%; Score 677; DB 6;
46.4%; Pred. No. 3.2e-39;
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EMBL; AF131883; AAF3817.1; -...
HSSP; Q00421; 1AMC.
Interpro; IPR002110; ANK.
Fran; PF00023; ank; 4.
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                                                                                                                                                                                                                                                                                  301 EHPEPESEQNGLERPG-SGRETPQPIPAQ 328
                                                                                                                                                                                                                                                              EHPEPGAEHNGLEGPNDSGRETPQPVPAQ 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        29 GDTRQKLPMDLLVLEDEKHHGAQSAALQKVI
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40.0%; S&
Best Local Similarity 46.4%; Pre
Matches 136; Conservative 54;
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                                                                                                                                                                                                                                                          121 GGACATGCTAGTGCTAGAGGAAGGAAGCGCCTCGGGGTTCAGAGGTCCTGGTTTACAAAA 180
                                                                                                                                                                                                                                                                                   ggtgaagggccaagagcgcgtgcgcaagacgtccctggacctgcgggggggagatcatcga 249
                                                                                                                                                                                                                                                                                                                                                                                                   tgaggaagaccttcctgaaagctgcggtggagggaaaatgaaggtcattgagaagttcct 429
                                                                                                                                                                                                                                                                                                                                                                                                                                                  gotggcacaggaggaggagtaggaaactccgaggagacacacgccagaagctgcccat 129
                                                                                                                                                    Gaps
                                                                                                                                                                    10 ggacggcackatggaggactccgaggcggtgcagaggccacagcgctcatcgagcagcg 69
                                                                                                                                                                                AKNLAGKTPTDLVQLWQADTRHALEHPEPESEQNGLERPGSGRETPQPIPAQ
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                                                                                                                                                   3;
                                                                                                                                 Length 1100;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                 DB 10;
                                                                                                                                                   191;
                                                                                                                                         Pred. No. 2e-136

 Mismatches

                                                                                                                                Score 759.4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                        ggctgacggggggtcagccgacacgtgcgaccagb
       455. .850
/rpt_family="Ankyrin"
/rpt_type=TaNDEM
998. .1100
/gene="Ankrd2"
1081. .1086
                                                                                           6
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                                                              /gene="Ankrd2"
1100
                                                                                  /gene="Ankrd2"
                                                                                                                                65.6%;
                                                                                          294 C
                                                                                                                                                   Conservative
                                                                                                                                           Similarity
                                                                                           a
                                                                                          284
        repeat_region
                                                       polyA_signal
                                                                                                                                          Best Local Sim
Matches 887;
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                                    'UTR
                                                                                          BASE COUNT
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Kemp, T.J., Sadusky, T.J., Saltisi, F., Carey, N., Moss, J., Yang, S.Y., Sassoon, D.A., Goldspink, G. and Coulton, G.R.
Identification of anixed, a novel skeletal muscle gene coding for a stretch-responsive anixed repeat protein
Genomics 66 (3), 229-241 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /translation="SAQEEENEKLRGDXRQKLPMDLLVLEDEKHHGAQSAALQKVKGQ
ERVRKTSLDLRREIIDVGGIQNLIELRKKRRQKKRDALAASHEPPPEPEEITGPVDEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (13-OCT-1999) Kemp T.J., Molecular Pathology, Imperial collage School OF Medicine, SAF Building Level 2, Exhibition Road, South Kensington, London, UNITED KINGDOM Related sequence: AJ245514.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Euteleostomi:
                                                                                                                              1029
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ankrd2 gene; ankyrin repeat domain 2; stretch responsive muscle
                                                                                                                                                                                                                             1077
                              900
                                                               696
                                                                                               957
                                                                                                                                                                                                                                                                                                                                                                            HSA249975 307 bp mRNA PRI 25-JUL-2000 Homo sapiens partial mRNA for ankyrin repeat domain 2 (stretch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                          1018 ACCCAACCCCCTACTATGAGCTGCCTGCAGCCCGTCTAGCAGGAACACCCCTAGATGCAA
                 1030 agctacccagcccctctctgtgtgcagccggagggtcctaagaatggctcccggagctaa
                                                                gcacgccctggagcatcctgagccgggggctgagcataacggggctggagggcctaatga
850 caagaacctggcaggaaagaccccgacggacctggtgcagctctggcaggctgatacccg
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
1 (bases 1 to 307)
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/protein_id="CAB99416.1"
/db_xref="GI:9501290"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /gene="ANKRD2"
7(1 .>30)
/gene="ANKRD2"
/note="stretch responsive muscle"
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Pred. No. 2.5e-48;
0; Mismatches 1;
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/db_xref="taxon:9606"
/tissue_type="skeletal muscle"
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                                                                                                                                                                                                                                                                                                                                                                                                           responsive muscle).
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Direct Submission
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Best Local Similarity 99.7
Matches 302; Conservative
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ORIGIN
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VERSION
KEYWORDS
SOURCE
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HSA249975
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AUTHORS
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JOURNAL
                                                               910
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FEATURES
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LAASHEPPPEPEETTGPVDEETFLKAAVEGKMKVIEKFLADGGSADTCDQFRRTALHR
ASLEGHMETLEKLLDNGATVDFQDRLDCTAMHWACRGGHLEVVKLLQSHGADTNVRDK
                                                         LLSTPLHVAVRTGQVEIVEHFLSLGLEINARDREGDTALHDAVRLNRYKIIKLLLHG
DADMTKNLAGKTPTDLVQLWQADTRHALEHPEPGAEHNGLEGPNDSGRETPQPVPAQ"
1664. . 6595
/gene-"ANKRD2"
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Pred. No. 1.3e-48;
0; Mismatches 1
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11111. .11209
/gene="ANKRD2"
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11210. .11399
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12659. .12664
/gene="ANKRD2"
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'gene="ANKRD2"
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'gene="ANKRD2"
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/gene="ANKRD2"
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ilarity 99.7%;
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HOMO sapiens ANKRD2 gene for skeletal muscle ankyrin repeat, exons
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 14300)
Pallavicini,A., Kojic,S., Bean,C., Vainzof,M., Salamon,M.,
Favolella,C., Bortoletto,G., Pacchioni,B., Trevisan,S.,
Faulkner,G., Lanfranchi,G. and Valle,G.
Characterization of human skeletal muscle Ankrd2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 (bases 1 to 14300)
Pallavicini,A.
Direct Submission
Submitted (18-DEC-2000) Pallavicini A., Biologia, Universita di Padova, via Ugo Bassi 58/b, 35100, ITALY
Location/Qualifiers
1. .14300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                oin(1567. .1663,6596. .6697,7036. .7194,7294. .7401,651. .9749,10112. .10210,11111. .11209,11400. .11498,2313. .12679)
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651. .9749,10112. .10210,11111. .11209,11400. .11498.
2373. .12522)
                                                     aagggccaagagcgcgtgcgcaagacgtccctggacctgcggcgggagatcatcgatgtg 253
                                                                                                                                                                        125 AAGGGCCAAGAGCGCGTGCGCAAGACGTCCCTGGACCTGCGGCGGGAGATCATCGATGTG 184
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ANKRD2 gene; skeletal muscle ankyrin repeat.
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538. .12679
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1567. 1667
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1538. .1542
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gene="ANKRD2"
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Ammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
(bases 1 to 163214)
12609 GCCCAGCCTTTTTTCTGCATGATCCAGGAGCACATACCACAACTACCACAATAAAAAA 12668
                                                                                                                                                                                                                                                                                                                                                                               AL355315 163214 bp DNA HTG 07-AUG-2001
Homo sapiens chromosome 10 clone RP11-548K23, *** SEQUENCING IN
PROGRESS ***, 3 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chapman J.
Direct Submission
Submitted (06-AUG-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 15A UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: Clonerequestssanger.ac.uk
On Aug 9, 2001 this sequence version replaced gi:15041819.
                                                                                                                                           1096 geocagecttttttetgeatgatecaggageacataceacaaactaceacaataaaaag 1155
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NOTE: This is a 'working draft' sequence. It currently consists of 3 contigs. The true order of the pieces is not known and their order in this gequence record is arbitrary. Gaps between the contigs are represented as runs of N but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                             1036 ccagccctctctgtgtgcagccggagggtcctaagaatggctcccggagctaactgagg
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Assembly program: XGAR4; version 4:5
Sequencing vector: plaAmid; L08752; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Consensus quality: 162660 bases at least 040
Consensus quality: 162660 bases at least 020
Insert size: 163014; sum-of-coatigs
Insert size: 169230; agarose-fp
Quality coverage: 10.60x in 020 bases; sum-of-contigs
coverage: 10.65x in 020 bases; agarose-fp
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42326 139511: contig of 97186 bp in length
139512 139611: gap of 100 bp
139612 163214: contig of 23603 bp in length.
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/db_xref="taxon:9606"
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Eukaryota; Metazoa; Chordata; Crahiata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 218959)
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                                                                                                                                                                                                                                                                                                                                                                                 856 octggkaggaaagaccccgacggacctggtgcagctctggcaggctgatacccggcacgc 915
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Direct Submission
Submitted (01-AUG-2001) Sanger Centre, Hinxton, Cambridgeshi
CEBO 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone
requests: clonerequest@sanger.ac.uk
On Jul 30, 2001 this sequence version replaced g1:15022209.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     916 cctggagcatcctgagccgggggctgagcataacgggctggaggggcctaatgatagtgg
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Sequencing vector: plasmid; L08752; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
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1. .4225
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//note-"assembly_fragment:02594
fragment_chain:1"
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0; Mismatches 1
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fragment_chain:1"
1 38587 c 39191 g 44022 t
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Web site: http://www.sanger.ac.uk
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Homo sapiens chromosome 10
PROGRESS ***, 15 unordered
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AL359388.21 GI:15041841
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AJ249975 Homo sapi AJ304804 Homo sapi AL355315 Homo sapi AL359388 Homo sapi AX140502 Sequence

AJ245514 Mus muscu AJ245514 Mus muscu

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X69063 M.musculus AF185591 Mus muscu

AE046089 Macaca fa AF105427 Homo sapi AR088277 Sequence AX025001 Sequence AF094760 Homo sapi

Res. Commun. (2001) In press

REFERENCE AUTHORS

SUMMARIES

JOURNAL

Perfect score:

Sequence:

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Database

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1 (sites)
Moriyama,M., Tsukamot,Y., Fujiwara,M., Kondo,G., Nakada,C.,
Moriyama,M., Tshiguro,N., Miyazaki,A., Nakamura,K., Hori,N., Sato,K.,
Shomori,K., Takeuchi,K., Satoh,H., Mori,S. and Ito,H.
Identification of a novel human ankyrin-repeated protein homologous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Homo saplens arpp mRNA for ankyrin-repeat protein, complete cds.
ABO58859
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AL391244
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2 (bases 1 to 1169)
Moriyama,M.
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Copyright (c) 1993 - 2000 Compugen Ltd.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo. I (bases 1 to 1159)
Pallavicini,A., Kojic,S., Bean,C., Vainzof,M., Salamon,M., Paulkner,G., Dartoletto,G., Pacchioni,B., Trevisan,S., Characterization of human skeletal muscle Ankrd2
Unpublished
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Pallavicini, A.
Direct Submission
Submitted (18-DEC-2000) Pallavicini A., Biologia, Universita di
Padova, via Ugo Bassi 58/b, 35100, ITALY
Location/Qualifiers
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Homo sapiens mRNA for skeletal muscle ankyrin protein 2 (ANKRD2
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ANKRD2 gene; skeletal muscle ankyrin protein
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Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 1100)
Kemp, T.J., Sadusky, T.J., Saltisi, F., Carey, N., Moss, J., Yang, S.Y., Sasson, D.A., Goldspink, G. and Coulton, G.R.

Gensson, D.A., Goldspink, G. and Coulton, G.R.

Identification of Ankrd2, a novel skeletal muscle gene coding for stretch-responsive ankyrin-repeat protein

Genomics 66 (3), 229-241 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (bases 1 to 1100)
Ievolella,C., Formentin,E. and Lanfranchi,G.
Characterization of a member of a new family proteins with ankyrin
                                                                                                                                                                           19-MAR-2001 cardiac protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Direct Submission
Submitted (30-SEP-1998) Ievolella C., CRIBI Biotechnology Cer
Universita di Padova, via G. Colombo 3 Padova, 35121, ITALIA
Related sequence F18281.
                                                       cggcacgccctggagcatcctgagccgggggctgagcataacgggctggaggggcctaat
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3 (bases 1 to 1100)
Ievolellà,C.
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                                                                                                                                                                                                                                                     Length 1159;
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6
                                                                                                                                                                                                                                                Score 1109.8; DB 9;
Pred. No. 8.1e-204;
1; Mismatches 3;
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Matches 1132; Conservative
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FEATURES
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EKRLGVQSPALOKVKGQERVRKTSLDLRREIIDVGGIQNLIELRKKFKQKKRDALAAA
QEPPPEPEBEITGPVNEETFLKAAVESKMKYIDKIAADGGSADTOBEFRYATALHRASLE
GHMEITEKLENGATVDFQDRLDCTPAHHWACRGGHLEVVRLLGSRGADTNVRDKLLST
PLHVAVRTGHYEIVBERFLSLGLDINKCNREGOSALHDAVRLNRYKIIKLLIHGADM
AKNLAGKTPTDLVQLWQADTRHALEHPEPESEGNGLERPGSGRETPQPIPAQ"
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                                                                                                                                                               10 ggacggcaccatggaggactccgaggcggtgcagagggccacagcgctcatcgagcagcg
                                         344.877

Anote—"contains ankyrin repeats and NLS (nuclear localization signal:KRRK) similar to C-193"

/rpt_family="ankyrin repeats"

/rpt_type="RANDEM"
998.1100
                                                                                                                                                 3;
                                                                                                                                 Length 1100;
                                                                                                                                                 Indels
                                                                                                                                 Score 761; DB 10;
Pred. No. 9.8e-137;
0; Mismatches 190;
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                                                                                                      181
                                                                                                      Б
                                                                                                      341
                                                                                                                                    Query Match 65.7%;
Best Local Similarity 82.1%;
Matches 888; Conservative
                                                                                                     293 c
                                                                                                1100
                                                                                                      285
                                                                                      polyA_signal
polyA_site
BASE COUNT 285
ORIGIN
                                             repeat_region
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/translation="MEGPEAVORATELIEORIAQEEETEKIERSAPGKLSMDMLVLEE"
KTRIGVOSPALOKVKGOERVRKTSLDIRREITDVGGGOLVLIEBIRKKKKGKRDALAAA
BERRLGVOSPALOKVKGOERVRKTSLDIRREITDVGGGONLIEBIRKKKKGKRDALAAA
GEPPEPEEETETTGPVNEEFETRAAVEGKWKVIDKYLAGGGSADTCDEERRTALHRASLE
GHMEILEKLIENGATVDFODREDCTAMHWACRGGHLEVVRLIGSRGADTNVRDKLLST
PLHVAVRTGHVEIVEHFLSLGILDINAKDREGDSALHDAVRLNRYKIIKLLILHGADDM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          l (bases 1 to 1100)
Kemp.T.J., Sadusky.T.J., Saltisi,F., Carey,N., Moss,J., Yang,S.Y., Sassoon,D.A., Goldspink,G. and Coulton,G.R. Identification of ankrd2, a novel skeletal muscle gene coding for genenics 66 (3), 229-241 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25-JUL-2000
2 (stretch responsive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kemp.T.J.
Direct Submission
Submitted (09-AuG-1999) Kemp T.J., Molecular Pathology, Imperial
Submitted (09-AuG-1999) Kemp T.J., Molecular Pathology, Imperial
College School Of Medicine, SAF Building, Exhibition Road, South
Kensington, London SW7 2AZ, UNITED KINGDOM
revised by author
                                                                                                                                                                                                                                            1018 acccaaccccracraráagcreccrecagccagrcragcaggaacaccccragargcaa 1077
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   responsive muscle.
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                                                                                                   1030 agctacccagccctct&tgtgtgcagcagcggaggtcctaagaatggctcccggagctaa
                                                                                                                                                                 gcacgcctggagcatcctgagccgggggctgagcataacgggctggaggggctaatga
gaggeteaacegetacaaaatcateaaactgetgeteetgeatggggetgacatgatgae
                                                                  caagaacctggcaggaaagaccccgacggacctggtgcagctctggcaggctgatacccg
                      MMD245514 1100 bp mRNA ROD
Mus musculus mRNA for ankyrin repeat domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  muscle).
AJ24514.1 GI:9501359
AD24514.2 GI:9501359
Ankrd2 gene; Ankyrin repeat domain; stretch
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /strain="C57BL/10"
/db_xref="taxon:10090"
/tissue_type="skeletal muscle"
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/product="ankyrin repeat
/protein_id="CAB99431.1"
/db_xref="G1:9901360"
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/organism="Mus musculus"
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/gene="Ankrd2"
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aknlagktptdlvqlwqadtrhalehpepeseqnglerpgscretpqp1paq'
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                                                                                                                                       3;
                                                                                                                     DB 10; Length 1100;
                                                                                                                                      Indels
                                                                                                                            Pred. No. 2e-136;
; Mismatches 191;
                                                                                                                     Score 759.4;
                                                                                    181
     455. 850

/rpt_family="ankyrin"

/rpt_type="ankyrin"

998. 1100

/gene="ankrd2"

1081. 1086

/gene="ankrd2"
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                                                                           /gene="Ankrd2"
                                                                                                                    Ouery Match 65.6%;
Best Local Similarity 82.1%;
Matches 887; Conservative (
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ERVRKTSLDLRREIIDVGGIQNLIELRKKRRQKKRDALAASHEPPPEPEEITGPVDEE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 307)
Sassoon, D. A., Goldspink, G. and Coulton, G.R.
Identification of ankrd2, a novel skeletal muscle gene coding for stretch-responsive ankyrin-repeat protein
Genomics 66 (3), 229-241 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Direct Submission
Submitted (13-OCT-1999) Kemp T.J., Molecular Pathology, Imperial
Submitted (13-OCT-1999) Kemp T.J., Molecular Pathology, Imperial
College School OF Medicine, SAF Building Level 2, Exhibition Road,
South Kensington, London, UNITED KINGDOM
Related sequence: AJ245514.
Location/Qualifiers
                                                                                                                            Ankrd2 gene; ankyrin repeat domain 2; stretch responsive muscle
                                                                                                                                                                                                                           1018 acccaacccctractargagcrgccrgcagccagrcraggaagaaccccragargcaa 1077
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n 2 (stretch
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               gcacgecetggagcatectgagecegggggetgagcataaegggetggaggggectaatga
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caagaacctggcaggaaagaccccgacggacctggtgcagctctggcaggctgatacccg
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Homo sapiens partial mRNA for ankyrin repeat domain
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Pred. No. 2.5e-48;
0; Mismatches 1; Indels
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/db_xref="taxon:9606"
/tissue_type="skeletal muscle"
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/translation="MDGTMEDSEAVORATALIEQRIAQEEENEKLRGDTRQKLPMDLL
VLEDEKHHGAQSAALQKVKGQERVRKTSLDLRREIIDVGGIONLIELKKRKQKRDA
LAASHEPPPEETITGPVBEFFLKAAVEKNKVTSKLEAGSAADTCDQFRTTALHR
SASHEGHMETIERLIDNGATVDFODRLDCTAMHWACRGGHLEVVKLLGSHGADTNVRDK
LLSTPLHVAYRTGQVEIVETYEFFLSLGLEINARDREGDTALHDAVRLNRYKIIKLLLGH
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12659. .12664
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7402. .9650
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/gene="ANKRD2
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/gene="ANKRD2
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/gene="ANKRD2"
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/gene="ANKRD2'
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/gene="ANKRD2"
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/gene="ANKRD2
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/gene="ANKRD2"
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/gene="ankkD2"
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Best Local Similarity 99.7%;
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Direct Submission

L Submitted (18-DEC-2000) Pallavicini A., Biologia, Universita di Submitted (18-DEC-2000) Pallavicini A., Biologia, Universita di Submitted (18-DEC-2000) Pallavicini A., Biologia, Universita di Padova, via Ugo Bassi 58/D, 35100, ITALY

1. 14300

/ Coganism="Homosapiens"

/ Ab_xref="taxon:9606"

/ Chromosome="10"

/ Ab_xref="taxon:9606"

/ Chromosome="10"

/ Gene="ANKRD2"

1538. 12679

/ gene="ANKRD2"
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Homo sapiens ANKRD2 gene for skeletal muscle ankyrin repeat, exons
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Bukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

1 (bases 1 to 14300)

Pallavicini,A., Kojic,S., Bean,C., Vainzof,M., Salamon,M.,

Paulavicini,A., Bortoletto,G., Pacchioni,B., Trevisan,S.,

Faulkner,G., Lanfranchi,G. and Valle,G.

Characterization of human skeletal muscle Ankrd2
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.9749,10112. .10210,11111. .11209,11400. .11498
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9651. 9749,10112. 10210,11111. 11209,11400.
12333. 12522)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      ANKRD2 gene; skeletal muscle ankyrin repeat.
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/gene="ANKRD2"
1567. 1663
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AJ304804.1 GI:11967780
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1. (bases 1 to 163214)
HTG 07-AUG-2001
HTG 07-AUG-2001
PROGRESS ***, 3 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Direct Submission
Submitted (06-AUG-2001) Sanger Centre, Hinxton, Cambridgeshire,
Submitted (06-AUG-2001) Sanger Centre, Hinxton, Cambridgeshire,
CB10 1SA, UR. E-mail enquiries: humquery@sanger.ac.uk
requests: clonerequestGsanger.ac.uk
On Aug 9, 2001 this sequence version replaced gi:15041819.
                                                                                                                                  1096 gcccagccttttttctgcatgatccaggagcacataccacaactaccacaataaaaag 1155
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Assembly program: XGAP4; version 4.5
Sequencing vector: plasmid; L08752; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Consensus quality: 162483 bases at least 040
Consensus quality: 162860 bases at least 030
Consensus quality: 162811 bases at least 020
Insert size: 163014; sum-of-contigs
Insert size: 169230; agarose-fp
Quality coverage: 10.60x in 020 bases; sum-of-contigs Quality
coverage: 10.65x in 020 bases; agarose-fp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  * arbitrary. Gaps between the contigs are represented as * runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence * as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                            HTG; HTGS_PHASE1; HTGS_ACTIVEFIN; HTGS_DRAFT; HTGS_FULLTOP
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42326 139511: contig of 97186 bp in length
139512 139511: gap of 100 bp
139512 163214: contig of 23603 bp in length.
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/db_xref="taxon:9606"
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 218959)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12527 CCAGCCCCTCTCTGTGTGCAGCCGGAGGGTCCTAAGAATGGCTCCCGGAGCTAACTGAGG 12586
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HOW Sapiens chromosome 10 clone RP11-445123, *** SEQUENCING IN PROGRESS ***, 15 unordered pieces.
AL359388
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submitted (01-AUG-2001) Sanger Centre, Hinxton, Cambridgeshire,
CB10 15A, UK. B-mail enquiries: humquery@sanger.ac.uk Clone
requests: clonerequest@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                          856 cctggcaggaaagaccccgacggacctggtgcagctctggcaggctgatacccggcacgc 915
                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        On Jul 30, 2001 this sequence version replaced g1:15022209.
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                                                                                                                                                                                                                                                                                                                               Length 163214;
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Sequencing vector: plasmid; L08752; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                 DB 2;
                                                                                             42326 ... 139511
/note="assembly_fragment:02594
fragment_chain:1"
139612. ... 163214
/note="assembly_fragment:00919
fragment_chain:1" 44022 t 21
a 38587 c 39191 g 44022 t 21
                                                                                                                                                                                                                                                                                                                               26.0%; Score 301.4; DB 2 99.7%; Pred. No. 7.2e-49; iive 0; Mismatches 1
/clone_lib="RPCI-11.2"
1. .42225
/note="assembly_fragment:05104
fragment_chain:1"
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Contact: humquery@sanger.ac.uk
------ Project Information
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Matches 302; Conservative
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us-09-758-593a-2.rge

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house mouse.

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Eukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus.

Mammalia; Eugheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 60 1758)

Wolf,E., Werner,S., Halle,J.P., Regenbogen,J. and Goppelt,A.

Use of polygetides or their encoding nucleic acids for the
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Location/Qualifiers
1. 1758
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Pred. No. 6.7e-49;
0; Mismatches 1;
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.218959
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52488 c 52339 g 57071 t 1
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Wassembly_fragment:07489
Ant_chain:4"
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t_chain:4"
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t_chain:3"
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-_chain:3"
.186875
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rom Patent EP1114862.
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Best Local Similarity 99.7%;
Matches 302; Conservatine (
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183156
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AX140502
                /note=
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      Consensus quality: 212933 bases at least 040 consensus quality: 214268 bases at least 030 consensus quality: 215362 bases at least 020 lineart size: 217559; sum-of-contigs of part size: 197049; la.4% error; agarose-fp lunity coverage: 9.97x in 020 bases; sum-of-contigs Quality coverage: 12.47x in 020 bases; agarose-fp
                                                                                                                                         * NOTE: This is a 'working draft' sequence. It currently consists of 15 contigs. The true order of the pieces is is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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211342 213521: contig of 2086 bp in length
213528 213572: gap of 100 bp
213528 215775: contig of 3148 bp in length
216775: contig of 3148 bp in length
216775 216875: gap of 100 bp
216876 218959: contig of 2084 bp in length.
Location/Qualifiers
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//note="assembly_fragment:04783
fragment_chain:1"
7456. 42891
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fragment_chain:1"
42992. 53582
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53683. 94414
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fragment_chain:1"
114544. .146062
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/note="assembly_fragment:00259
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/clone="RR11 445123"
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114544 146062: contic
146063 146162: gap of
146163 176482: contic
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/organism-"Mus musculus"
                                               /db_xref="taxon:10090"
                                                 /tissue_type="heart"
15. .974
           Location/Qualifiers
                                                                       Similarity
92093,
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Matches 381;
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200, Y., Evans, S., Chen, J., Kuo, H.C., Harvey, R.P. and Chien, K.R. CARP, a cardiac ankyrin repeat protein, is downstream in the Nkx2-5 homeobox gene pathway
Development 124 (4), 793-804 (1997)
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Chen,J. and Chitan K.R.
Direct Submission
Submitted (07-JAN-1998) Medicine, UCSD, 9500 Gilman Dr, La Jolla,
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Mus musculus cardiac ankyrin repeat protein MCARP mRNA, complete
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                                                                        Score 264.8; DB 6;
Pred. No. 2.3e-41;
0; Mismatches 197;
                         u
                         391
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364 c 450 g 391
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                                                                        22.9%;
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LLTALHVANGTGKTPMDLYLACEADLMAKDREGDFPLHDAVRLNRTKMIRLLMTFGA
LLTALHVANGAGTAAIPGSPKENAXFNSRIATF"

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                                                                                                                                                                                                                                                                                                                                                                                               328 tgagccgccccagagcccgaggagatcactggccctgtggatgaggagaccttcctgaa 387
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                                                                                                                                                                                                                                                                                                        Length 1026;
/product-"cardiac ankyrin repeat protein MCARP"
/protein_id="AAC03533.1"
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65.7%; Pred. No. 1.1e-40;
iive 0; Mismatches 199;
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gacccgacggacctggtgcagctctggcaggctgatacc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /product="nuclear protein"
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/chromosome="l0"
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/cell_type="endothelial"
/clone_lib="HDMEC_CDNA"
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milarity 64.7%;
Conservative 0
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Matches 369; Conserv
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IKTANSVNLGEEDGEKSEKVREABELKKKLEORSKLENLEDLEIIVQLKKRKKKKKT
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DLNVKNCAKFROAKTGHYEGABLILACEADLINAKOREGDTPLHDAVRLNKKMIRLLMTFGA
DLNVKNCAKFROAKFRONGTKAIFDSLKENAYKNSRIATF"
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0
                                                                       Jeyaseelan, R., Poizat, C., Abdishoo, S. and Kedes, L. Jeyaseelan, Birect Submission and Molecular Submitted (05-MAR-1996) R. Jeyaseelan, Biochemistry and Molecular Biology, University of Southern California, School of Medicine, 2011, Zonal Ave, HMR 413, Los Angeles, CA 90033, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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                                                                                                                                                                                                                                  /note="Cardiac Adriamycin Responsive Protein,
transcription factor"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                     /organism="Rattus norvegicus"
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Pred. No. 8.1e-40;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 22.2%;
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Best Local Similarity
Matches 378; Conserv
           Norway rat
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1 (bases 1 to 1901)
Chu, W., Burns, Dg.K., Swerlick, R.A. and Presky, D.H.
Identification and characterization of a novel cytokine-inducible nuclear protein from human endothelial cells
J. Biol. Chem. 270 (17), 10236-10245 (1995)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (05-JAN-1995) W. Chu, Hoffmann-La Roche, 340 Kingsland Street, Dept. of Inflammation/Autoimmune Disease, Hoffmann-La Roche, Nulley, NJ 07110, USA Location/Qualifiers
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H.sapiens mRNA for cytokine inducible nuclear protein.
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Pred. No. 3.3e-38;
0; Mismatches 201;
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KCl:
Tris-HCl:
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Matches 369; Conservative
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           Buffer:
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primer_bind
BASE COUNT 59
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

I (bases 1 to 1901)
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                                               gagaagettetagataatggggeeactgtggaetteeaggateggetggaetgeacagee
                                                           atgcattggggcctgccgcgggggccacttagaggtggtaaacttctgcaaagccatgga
                                                                                                                     817 ATCCACTGGGCAAGCCGTGGAGGAAACCTGGATGTTTTAAAATTGTTGCTGAATAAAGGA
gaccagttccgtcggacagcactgcaccgagcttccctggaaggccacatggaaatcctg
                     697 GATGAGTATAAACGGACAGCTCTTCATAGAGCATGCTTGGAAGGACATTTGGCAATTGTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Richard M. Myers
Stanford Human Genome Center (SHGC)
Stanford University School of Medicine
Department of Genetics, M-344, Stanford, CA 94305, USA
Tel: 4157259687
Fax: 4157259689
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             degrees C for 15 s degrees C for 23 s degrees C for 30 s
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 G28603.1 GI:1408418
STS; STS sequence; primer; sequence tagged site.
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62 degrees C for 23
72 degrees C for 30
30
Perkin Elmer 9600
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human STS SHGC-35401, sequence tagged site.
G28603
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each 1 uM
each 200 uM
0.05 units/ul
10 ul
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222
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Thermal Cycler:
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Polymerization:
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Profile:
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                                                             Prepared with primer pairs provided by Sandoz, derived from X83703
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                                                                          Washington University/Merck EST sequence
Location/Qualifiers
                                                                                                                                                                                                                                          21.5%; Score 248.4; DB 11;
64.7%; Pred. No. 3.3e-38;
iive 0; Mismatches 201;
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                                                                                                 1. .1901
/organism="Homo sapiens"
/db_xref="taxon:9606"
/map="10"
1246. .1467
1246. .1263
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AJ249346.1 GI:9501361
Ankrd2 gene; ankyrin repeat domain
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                       907
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373. .9733
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                         gacctggtgcagctctggcaggctgatacc
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573. .578
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/gene="Ankrd2"
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/gene="Ankrd2"
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LKTLPAHHVSLAEQQWEREKQLEAELKKKKLEQRSKLENLEDLEIIIQLKKKKKYRKT
KVPVAKEPREDITTEPVDVPRFLKAALENKLAVVEKFLSDQNBDVCDEYKRTAHRA
LEGGHLALVEKLMEAGADIEFDMLESTAIHWACRGGNLEVLKLLLAKGAKISARDKK
LSTALHVAVRTGHTEAEDAELIACEADLNAKDREGDTPLHDAVRLNRYKMIKLIMYGA
DLITKRAGKRPPMDLVLNWQNGTKAIFDSLKENSYKTSRIATF"
391 c 479 g 447 t
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                                (bases, ltoll), Aral, M., Aral, M., Kedes, L. and Nagal, R. Malecular cloning of rabbit CARP cDNA and its regulated expression in adriamycin-cardiomyopathy
Biochim. Blophys. Acta 1447 (2-3), 318-324 (1999)
                                                                                                                                                                          Direct Submission
Submitted (26-FEB-1999) Second Department of Internal Medicine,
Gunma University School of Medicine, 3-39-15 Showa-machi, Maebashi
        Oryctolagus cuniculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus
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Pred. No. 2.7e-37;
0; Mismatches 204;
                                                                                                                                                                                                                                              /organism="Oryctolagus cuniculus"
/db_xref="taxon:9986"
219. .1178
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/db_xref="G1:6478317"
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Best Local Similarity 64.2%;
Matches 366; Conservative
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Aihara, Y.
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AKNLAGKTPULVQLWQADTRHALEHPEPESEQNGLERPGSGRETPQPIPAO"
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/note=rea relains 129/SvevTACfBr, C57BL/6 and C57BL/10"
/rpt_family="Ca repeat"
/rpt_unit=1020. 1021
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6994. .7092,8376. .8474,8666. .8764,9484. .9733)
//ene="Ankrd2"
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6994. .7092,8376. .8474,8666. .8764,9484. .9630)
/gene="Ankrd2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kemp, T.J., Sadusky, T.J., Saltisi, F., Carey, N., Moss, J., Yang, S.Y., Sassoon, D.A., Goldspink, G. and Coulton, G.R.
Identification of ankrd2, a novel skeletal muscle gene coding for stretch-responsive ankyrin-repeat protein
Genomics 66 (3), 229-241 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Direct Submission
Submitted (09-SEP-1999) Kemp T.J., Molecular Pathology, Imperial
Submitted (09-SEP-1999) Kemp T.J., Molecular Pathology, Imperial
College School Of Medicine, SAF Building, Exhibition Road, South
Kensington, London SW7 2AZ, UNITED KINGDOM
                                                                                                                                                                                                                                                                                                                                                                                                                                            2; stretch responsive muscle.
25-JUL-2000
domain 2 (stretch
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9
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4889 ACAGATGTGGGCAGGGGAGCCTGGGAGGCCCGGAAGCTCCTTTATTGGCGG 4948

435 acggggggtcagccgacacgtgcgaccagttccgtcggacagcactgcaccgagcttccc 494

375 agaccttcctgaaagctgcggtggaggggaaatgaaggtcattgagaagttcctggctg 434

Search completed: April 17, 2002, 10:07:55 Job time: 7119 sec

Title: Perfect score:

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Q94f4 homo sapien
Q97d7 homo sapien
Q97d7 homo sapien
Q97d8 drosophila
Q97sa drosophila
Q97sa drosophila
Q9x23 drosophila
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Q94d8 mus musculu
Q9137 mus musculu
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Q1295 homo sapien
Q94uy drosophila
Q9vus drosophila
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Ievolalla C., Borjic S., Bean C., Vainzof M., Salamon M.,
Ievolalla C., Borjic S., Bean C., Vainzof M., Faulkner G.,
Lanfranchi G., Walle G.,
"Characterization of human skeletal muscle Ankrd2.";
Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ304804; CAC19412.1;
InterPro: IPR002110; ANK.
Figm. PF00023; ank.
Prim. PF00023; ank.
SMART; SM00248; ANK; 5.
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01-JUN-2001 (TIEMBLIE]. 17, Last annotation update)
SKELETAL MUSCLE ANKYRIN PROTEIN 2 (SKELETAL MUSCLE ANKYRIN REPEAT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 100.0%; Score 1693; DB 4; Length 333; Best Local Similarity 100.0%; Pred. No. 3e-109; Matches 329; Conservative 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         679736F0491467A8 CRC64;
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PROSITE: PS50297; ANK_REP_REGION; 1.
SEQUENCE 333 AA; 37151 MW; 67973
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Q9ERD4
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01-MAR-2001 (TrEMBLrel. 16,
01-MAR-2001 (TrEMBLrel. 16,
01-JUN-2001 (TrEMBLrel. 17,
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            RESULT
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09nq99 homo sapien
09vux2 drosophila
095271 homo sapien
091qp7 arabidopsis
091qp7 arabidopsis
                                                                                                                                                                                                                                                                              April 17, 2002, 08:10:37; Search time 26.67 Seconds (without alignments) 1804.409 Million cell updates/sec
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O55014 mus musculu
Q9cr42 mus musculu
Q15327 homo sapien
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Q9wv06 mus musculu
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                                              GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             473505 seqs, 146272329 residues
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Maximum Match 100%
Listing first 45 summaries
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Q9WV06
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Gapop 10.0 , Gapext 0.5
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sp_unclassified:*
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sp_human:*
sp_invertebrate:*
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Maximum DB seq length: 200000000
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sp_bacteria:*
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sp_virus:*
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Q9has4 homo sapien

091vg7 arabidopsis 09v4b1 drosophila

Q9N180 Q9LVG7 Q9V4B1 Q9H0I4 Q9J4Z4

1166 1265 1050 592 1136 548 1549

244 241.5 241.5 240.5 239.5

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   185 TAMHWACRGGHLEVVKLLQSHGADTNVRDKLLSTPLHVAVRTGQVEIVEHFLSLGLEINA 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EINARDREGDTALHDAVRLNRYKIIKLLLLHGADMMTKNLAGKTPTDLVQLWQADTRHAL 300
RLDCTAMHWACRGGHLEVVKLLQSHGADTNVRDKLLSTPLHVAVRTGQVEIVEHFLSLGL
                                                                                                                                                                                                                                                                                                                                                              Euteleostomi;
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                                                                                                                                                                                                                                                                                                                                                                                                                REQUENCE FROM N.A.

P. SEQUENCE FROM N.A.

MEDLINE-20011295; Pubmed=10542334;

A Albara Y., Kurabayashi M., Arai M., Kedes L., Nagai R.;

A Albara Y., Kurabayashi M., Arai M., Kedes L., Nagai R.;

Molecular cloning of rabbit CARP cDNA and its regulated expi
adriamycin-cardiomyopathy ";

E Biochim. Biophys. Acta 1447:318-324(1999).

R BHSSP: Q00421; LMW.

R HSSP: Q00421; LMW.

R FFSP: PR00218; ANK. 4.

Pfam: PF00023; ANK. REPEAT; 4.

R PROSTITE; PS50209; ANK. REPEAT; 4.

R PROSTITE; PS50209; ANK. REPEAR; CTEF87A02936FED3 CRC64;

SEQUENCE 319 AA; 36245 MW; CTEF87A02936FED3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 319;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                  C.....
Divertolagus cuniculus (Rabbit).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eut
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
                                                                                                                                                                                                                                                                                         01-MAY-2000 (TrEMBLrel, 13, Created)
01-MAY-2000 (TrEMBLrel, 13, Last sequence update)
01-JUN-2001 (TrEMBLrel, 17, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 40.0%; Score 677; DB 6; L4
46.4%; Pred. No. 3.2e-39;
Live 54; Mismatches 69;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        29 GDTRQKLPMDLLVLEDEKHHGAQSAALQKVKGQE-----
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                                                                                                                                                                                EHPEPESEQNGLERPG-SGRETPOPIPAQ 328
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                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=9986;
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Best Local Simi
Matches 136;
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Q9TU71;
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ID 09
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121 FLKAAVEGKMKVIEKFLADGGSADTCDQFRRTALHRASLEGHMEILEKLLDNGATVDFQD 180
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                                                                                                                                                            FLKAAVEGKMKVIEKFLADGGSADTCDQFRRTALHRASLEGHMEILEKLLDNGATVDFQD 180
                                                           184
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STRAIN-WARDINGS STRAINS; TISSUE-SPLEEN, AND SKELETAL MUSCLE;
Kemp T.J., Sadusky T.J., Saltisi F., Carey N., Moss J., Yang S.Y.,
Sassoon D.A., Goldspink G., Coulton G.R.;
Tidentification of Ankrd2, a novel skeletal muscle gene coding for
stretch-responsive ankyrin-repeat protein.";
Genomics 66:229-241(2000).
EMBL, AJ1249346; CAB46646.1;
EMBL, AJ249346; CAB99431.1;
EMBL, AJ24514; CAB99431.1;
EMBL, AJ24534; CAB99431.1;
EMBL, AJ24534; CAB99431.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          revolella C., Formentin E., Lanfranchi G., "The serication of a member of a new family proteins with ankyrin "Characterization of a member of a new family proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MEDSEAVORATALIEORLAGEEENEKLRGDTROKLPMDLLVLEDEKHHGAGSAALQKVKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Craniata; Vertebrata; Buteleostomi;
Sciurognathi; Muridae; Murinae; Mus.
                                               EINARDREGDTALHDAVRLNRYKIIKLLLHGADMMTKNLAGKTPTDLVQLWQADTRHAL
                                                                                        RLDCTAMHWACRGGHLEVVKLLQSHGADTNVRDKLLSTPLHVAVRTGQVEIVEHFLSLGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             87.7%; Score 1484.5; DB 11; Length 328;
88.8%; Pred. No. 7.1e-95;
ive 14; Mismatches 22; Indels 1;
                                                                                                                                                                                                                                                                                                                                  01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-NOV-1999 (TrEMBLrel. 17, Last annotation update)
skeletal MUSCLE AND CARDIAC PROTEIN (ANKYRIN REPEAT DOMAIN 2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              repeats.";
Submitted (SEP-1998) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PS5008; ANK_REPEAT; 4.
PS50297; ANK_REP_REGION; 1.
328 AA; 36707 MW; DB90D955EE9D175E CRC64;
                                                                                                                                                                                                                                                                                                             328 AA
                                                                                                                                                                                                          301 EHPEPGAEHNGLEGPNDSGRETPQPVPAQ 329
                                                                                                                                                                                                                         EHPEPGAEHNGLEGPNDSGRETPQPVPAQ 333
                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MGD; MGI:1861447; Ankrd2.
InterPro; IPR002110; ANK.
Pfam; PF00023; ank; 4.
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-TISSUE=DIAPHRAGM MUSCLE;
                                                                                                                                                                                                                                                                                                                PRELIMINARY;
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Best Local Similarity
Matches 292; Conserv
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PROSITE; 1
SEQUENCE
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Q9WV06;
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Q9WV06
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                                                                                                                                                                                                                                                                                                                                                                                                           SADTCDQFRRTALHRASLEGHMEILEKLLDNGATVDFQDRLDCTAMHWACRGGHLEVVKL 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE-HEART;
MEDLINE-97195688; PubMed-9043061;
Zou Y., Evans S., Chen J., Kuo H.C., Harvey R.P., Chien K.R.;
"CARP, a cardiac ankyrin repeat protein, is downstream in the Nkx2-5
                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                   22 EENEKLRGDTRQKLPMDLLVLEDEKHHGAQSAALQKVKGQERVRKTSLDLRREIIDVGGI 81
                                                                                                                                                                                                                                                                                                                                       40 EKQEDLK-----TLPANSVNLGEEQRKS-----EKVREAE-LKKKKLEQRSKLENLEDL 87
                                                                                                                                                                                                                                                                                                                                                                                                                        LQSHGADTNVRDKLLSTPLHVAVRTGQVEIVEHFLSLGLEINARDREGDTALHDAVRLNR
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                              15;
                                                                                                                                                                                                                                                                     Score 669.5; DB 11; Length 319;
Pred. No. 1e-38;
5; Mismatches 81; Indels 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    262 YKIIKLLLLHGADMMTKNLAGKTPTDLVQLWQADTRHALEHPEPGAEHN 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                265 YKMIRLLMTFGADLNVKNCAGKIPMDLVLHWQNGTKAIFDSLKENAYKN 313
                                                                                                                               Jeyaseelan R., Poizat C., Abdishoo S., Kedes L.;
Submitted (MAR-1996) to the EMBL/GenBank/DDBJ databases.
EMBL; U50736; AAD10401.1; -.
HSSP; Q00421; IAWC.
                                                                                                                                                                            InterPro: IPR00110; ANK.
Pfam; PF00023; ank; 4.
SMART; SM00248; ANK; 4.
PROSITE; PS50029; ANK_REPEAT; 4.
SROUTE; PS50297; ANK_REP_REGION; 1.
SEQUENCE 319 AA; 36075 MW; F78EB18BFD6049E0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-JUN-1998 (TrEMBLrel. 06, Created)
01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
         01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CARDIAC ANKYRIN REPEAT PROTEIN MCARP
                                                                                                                                                                                                                                                         39.5%; Scut-
47.4%; Pred
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Development 124:793-804(1997).
                                                                                                                                                                                                                                                                                            Matches 137; Conservative
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                                                       Rattus norvegicus (Rat).
                                                                                                                         STRAIN-SPRAGUE-DAWLEY;
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                                                                                                                                                                                                                                                                                  Local Similarity
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                                                                                                             SEQUENCE FROM N.A.
                                                                                       NCBI_TaxID-10116;
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055014;
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MEDLINE=2108560; PubMed=11217851;

MEDLINE=2108560; PubMed=11217851;

MEDLINE=2108560; PubMed=11217851;

A ARAWA T., Hara A. Fukunishi Y., Konno H., Adachi J., Fukuda S.,

A Azawa K., Izawa M., Nishi K., Kiyosawa H., Rondo S., Yamanaka I.,

A Azawa K., Izawa M., Nishi K., Kiyosawa H., Rondo S., Yamanaka I.,

A Azawa K., Izawa M., Nishi K., Kiyosawa H., Rondo S., Yamanaka I.,

RAGOLA K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

RAGOLA K., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

Ruchl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

Schriml L.M., Staubli F., Suzuki R., Tomita M., Magner L., Washio T.,

Baka J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,

Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,

Brownstein M.J., Bult C., Fletcher C., Fluita M., Garibodid M.,

Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           154 LHRASLEGHMEILEKLLDNGATVDFQDRLDCTAMHWACRGGHLEVVKLLQSHGADTNVRD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         214 KLLSTPLHVAVRTGQVEIVEHFLSLGLEINARDREGDTALHDAVRLNRYKIIKLLLLHGA
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       39.4%; Score 667; DB 11; Length 319; 47.3%; Pred. No. 1.6e-38; ive 55; Mismatches 77; Indels 1.
                                                                                                                             Schoenfeld J.R., Lowe D.G., Zou Y., Chen J.;
Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AF041847; AAC03533.1; -.
EMBT; AF041849; AAB97080.1; -.
Chen J., Chien K.R.;
Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE; PS50068; ANK_REPEAT; 4.
PROSITE; PS50297; ANK_REP_REGION; 1.
SEQUENCE 319 AA; 35939 MW; 6849DE07FD80517B CRC64;
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01-JUN-2001 (TIEMBLrel. 17, Last sequence update)
01-JUN-2001 (TIEMBLrel. 17, Last annotation update)
ANKYRIN-LIKE REPEAT PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            274 DMMTKNLAGKTPTDLVQLWQADTRHALEHPEPGAEHN 310
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                                                                                                       SEQUENCE OF 103-176 FROM N.A.
                                                                                                                                                                                                                                                                     HSSP; 000421: 1AWC.
MGD: MGI:109621: ALrp.
InterPro: IPR002110; ANK.
Pfam: PF00023: ank: 4.
SMART; SM00248; ANK: 4
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292 VLHWQNGTK 300
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             Query Match
Best Local Similarity
Matches 129; Conserv
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SEQUENCE
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Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F., Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L., Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Rohtsuki S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chu W., Burns D.K., Swerlick R.A., Presky D.H.;

"Identification and characterization of a novel cytokine-inducible nuclear protein from human endothelial cells.";

"J Biol. Chem. 270:10236-10245(1995).

EMBL: X83703; CAA58676.1; -..

HSSP; Q00421: IAMC.

Ffan; PF00023: ank; 4.

SMART; SM00248: Ank; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EKHHGAQSAALQKVK-GQER-----VRKTSLDLRREIIDVGGIQNLIELRKKRKQ 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1996 (TrEMBLrel. 17, Last annotation update)
NUCLEAR PROTEIN.
Homo sapiens (Human).
How sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Wynshaw DOLD ...,

**Wynshaw DOLD ...,

**Punctional annotation of a full-length mouse cDNA collection.";

**EMBL; AK009655; BAB26611.1; -

**EMBL; AK009655; BAB26419.1; -

**MGD; MGI: 1096212; AlrP.

**MGD; MGI: 1096212; AlrP.

**FROSITE; PSO0023; ann; 4

**SMART; SM00248; ANK; 4

**SMART; SM00248; ANK, REPEAT; 4.

**PROSITE; PSSO039; ANK, REP. REGION; 1.

**PROSITE; PSSO039; ANK, REP. REGION; 1.

**SEG0297; ANK, REP. REGION; 1.

**SEG0297; ANK, REP. REGION; 1.

**SEG0207CE ..., 36003 MM; 26A3C4062CF0E7D0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 319;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             319 AA; 36221 MW; 9C6E1D2B1C14A235 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Score 666; DB 11;
; Pred. No. 1.8e-38;
54; Mismatches 77;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; 274 DMMTKNLAGKTPTDLVQLWQADTRHALEHPEPGAEHN 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ΑA
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PROSITE; PS50297; ANK_REP_REGION; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             39.3%;
illarity 47.7%;
Conservative 5
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SEQUENCE FROM N.A.
TISSUE=SKIN;
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SEQUENCE 319 A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      132;
                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
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Matches 13
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OQ1532
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                                                                                                                                                                                                                     FSLDLRREIIDVGGIQNLIELRKKRKQKKRDALAASHEPPPE 108
                                                                                                  SGKMKVIEKFLADGGSADTCDQFRRTALHRASLEGHMEILEK 168
                                                                                                               228
                                                             TISSUE-SKELETAL MUSCLE:
TISSUE-SKELETAL MUSCLE:
MEDLINE-20334618: PUBMed-10873377;
MEDLINE-20334618: PUBMed-10873377;
Sassoon D.A., Goldspin G., Coulton G.R.;
Tidentification of Apmrd2, a novel skeletal muscle gene coding for stretch-responsive apmyrin-repeat protein.";
Genomics 66:229-241(2000).
EMBL; AJ249975; CAB99016.1; -.
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මුimates; Catarrhini; Hominidae; Homo.
                                                                                                                                                     MHWACRGGHLEVVKLLQSHGADTNVRDKLLSTPLHVAVRTGQ
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Length 319;
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                                                                                                                                                                                                                                                                                                                                                                                               15, Last sequence update)
15, Last annotation update)
(FRAGMENT).
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Last sequence update)
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Pred. No. 5.4e-28;
  ; DB 4;
6.5e-38;
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                                                                                                                                                                                                                                                                                                                                                             102 AA
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9%; Score 658; DE 8%; Pred. No. 6.56
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01-MAY-2000 (TrEMBLEEL 13,
01-MAY-2000 (TrEMBLEEL 13,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            29.8%;
99.0%;
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01-007-2000 (Tremblice) 1
01-007-2000 (Tremblice) 1
ANKYEN REPEAT DOMAIN 2
     38.9
nilarity 51.8
Conservative
                                                                                                          GEOOWKSEKOREAE-LPK
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                                                                                                                                                                                                                  229 VEIVEHFLSLGLEINARD
                                                                                                                                                                                                                                                                                                                                                                  PRELIMINAR
                                                                                                                                                                 LLDNGATVDFODRLDCT
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Best Local Similarity
Matches 100; Conservaë
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GGIONLIELRKKRKO
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens (Human);
Eukaryota; Metazoa; Cd
Mammalia; Eutheria; Pa
NCBI_TaxID=9606;
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                                                         GAQSAALQKVKGQERVR
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172 LMEAGAQIEFRDMLEST
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197

PRT; 1327 AA.

PRELIMINARY;

---PEEITGPVDEETFLKAAVEGKMKVIEKFLADGGSADTCDQ---

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440 ORGHGEWADAMOLTLGKIGRVQQVYHDNDLKVEVGNTSWTYNPLAVCKVASSTASDGSCA 499
                                                                                                                                                       149 -----FRRTALHRASLEGHMEILEKLLDNGATVDFQDRLDCTAMHWACRGGHLE
                                                                                                                                                                                    500 PVIPSSERLSAILKKLFEPNVSGDATEE-FVKAAANGFAARCEEYLAGAAQPSTSSASPS
                                                                                                                                                                                                                                                          198 VVKLLQSHGADTNVRDKLLSTPLHVAVRTGQVEIVEHFLSLGLEINARDREGDTALHDAV
                                                                                                                                                                                                                                                                                                                                                                                         679 SKEHDEMLSLLLDFGADITLNNNG 703
                                                                                                                                                                                                                                                                                                                                                            258 RENRYKIIKLLLHGADMMTKNLAG 282
                                                     102 SHEPPPE-----
                                                                                                                                                                                                                                                                                                          Dp
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                                                                                                                                                                                                                                                                  RECORD REPORT STAIN STAI
                                  Drosophila melanogaster (Fruit fly).
Bukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pteryota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PS50297; ANK_REP_REGION; 1.
1214 AA; 128461 MW; 53CC2D132B7CA471 CRC64;
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRINTS; PRO1415; ANKYRIN.
SWART; SM00248; AIK; 7.
SMART; SM00184; RING; 3.
SWART; SM00291; ZnE_ZZ; 1.
PROSITE; PS50088; ANK_REPEAT; 6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Flybase; FB900036558; CG5841.
InterPro; IPR002110; ANK.
InterPro; IPR001841; Znf_ring.
InterPro; IPR000433; ZnF_ZZ.
Pfam; PF00023; ank; 8.
Pfam; PF00569; ZZ; 1.
                                                                                                                                                                                                                               SEQUENCE FROM N.A. STRAIN-BERKELEY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
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575
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        635
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -----TAMHWACRGG 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 636 QQILSESTPIRTSDVDYRLLEASKAGDLETVKQLCSSQNVNCRDLEGRHSTPLHFAAGYN 695
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels 113; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         40 LVLEDEKH---HGAQSAALQKVKGQERVRKTSLDLRREIIDVGGIQN-----LIELR 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         576 VLHKHGAKMNALDTLGOTALHRAALAGHLQTCRLLLSYGSDPSIISLQGFTAAQMGNEAV
01-MAY-1999 (TrEMBLrel. 10, Created)
1-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-MAY-2001 (TrEMBLrel. 17, Last annotation update)
1-UNY-2001 (TrEMBLrel. 17, Last annotation update)
TRF1-INTERACTING ANKYRIN-RELATED ADP-RIBOSE POLYMERASE.
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhin; Hominidae; Homo.
                                                                                                                                                                                                                                                                      TISSUE=TESTIS;
MEDLINE=99040105; PubMed=9822378;
Smith S., Girlat I., Schmitt A., de Lange T.;
Smith S., Girlat I., Schmitt A., de Lange T.;
Schence 282:1484-1487(1998).
EMBL; AF082556; AAC79841.1; -.
EMBL; AF082557; AAC79842.1; -.
HSSP; P42771; 1B17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 1327;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PS50088; ANK_REPEAT; 15.
PROSITE; PS50297; ANK_REP_REGION; 1.
SEQUENCE 1327 AA; 142010 MW; E14DE985C710B957 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               135 KFLADGGSADTCDQFRRTALHRASLEGHMEILEKLLDNG------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14.7%; Score 249.5; DB 4; 26.2%; Pred. No. 5.8e-09; iive 33; Mismatches 110;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 26.2%
Matches 91; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR002110; ANK.
InterPro; IPR001660; SAM.
Pfam; PF00023; ank; 18.
Pfam; PF00536; SAM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRINTS; PR01415; ANKYRIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SMART; SM00248; ANK; 15.
SMART; SM00454; SAM; 1.
                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                             NCBL_TaxID=9606;
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6

5;

Gaps

28;

EKHHGAQSAALQKVKGQ-ERVRKT--SLDLRREIIDVGGIQNLIELRKKRKQKKRDALAA 101

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45

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16.3%; Score 276; DB 5; Length 1214; 29.8%; Pred. No. 7.7e-11; ive 42; Mismatches 116; Indels 2

Query Match
Best Local Similarity 29.8
Matches 79; Conservative

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Theologis;
                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q9H2K2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   62
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Q9H2K2
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δλ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Arabidopsis thaliana (Mouse-ear cress).
Arabidopsis thaliana (Mouse-ear cress).
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                          SECUENCE FROM N.A. SECUENCE FROM M.A. Tanuma R., Iseki K., Hirai M., Terao K., Suzuki Y., Sugano S., Hashimoto K.; "Isolation of full-length cDNA clones from macaque brain cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         211 VRDKLLSTPLHVAVRTGQVEIVEHFLSLGLEINARDREGDTALHDAVRLNRYKIIKLLL 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .....LDCTAMHWACRGGHLEVVKLLQSHGADTN 210
                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                        696 RVSVVEYLLHHGADVHAKDKGGLVPLHNACSYGHYEVAELLVRHGASVNVADLWKFTPLH 755
                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAVEGKMKVIEKFLADGGSADTCDQFRRTALHRASLEGHMEILEKLLDNGATVDFQDR--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     109 NTALHEASWHGFSQSAKLLVKAGANVLAKNKAGNTALHLACQNSHSQSTRVLLLAGSRAD
                                                                                                                                                                               Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
Cercopithecinae; Macaca.
             195 HLEVVKLLQSHGADTNVRDKLLSTPLHVAVRTGQVEIVEHFLSLGLEINARDREGDTALH
                                                                                                                                                                                                                                                                                                                                                                                                                                     33;
                                                                                                                                                                                                                                                                                                                                                                                                                 DB 6; Length 307;
                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                       libraries.";
Submitted (JUL_2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AB046089; BAB01671.1; -.
InterProvo; IPR002110; ANK.
Pfam; PF00023; ank; 7.
SMART; SM00248; ANK; 6.
                                                      DAVRLNRYKIIKLLLLHGADMMTKNLAGKTPTDLVQLWQADTRHALE 301
                                                                    D8E6EF1994504B95 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Last sequence update)
Last annotation update)
                                                                                                                                                      01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                 14.7%; Score 248.5; DB 6; 31.0%; Pred. No. 1.1e-09; 11ve 32; Mismatches 71;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             543 AA.
                                                                                                                                   Ą
                                                                                                                                  307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Created)
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                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                 PROSITE; PS50088; ANK REPEAT; 6. PROSITE; PS50297; ANK_REP_REGION; SEQUENCE 307 AA; 32684 MW; D8E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-OCT-2000 (TrEMBLrel. 15, C1 01-OCT-2000 (TrEMBLrel. 15, L2 01-UN-2001 (TrEMBLrel. 17, L4 F2489.19 PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   271 HGADMMTKNLAGKTPTD 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q9LQP7;
01-0CT-2000 (TrEMBLrel.
                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                           61;
                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local S
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                                                                                                                                    Q9N043
Q9N043;
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                                                                                                                RESULT 11
                                                             255
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61
STRAIN-CV. COLUMBIA:
Liu S., Yu G., Sakano H., Jhaveri A., Lee J., Lenz C., Pham P.,
Liu S., Yu G., Sakano H., Jhaveri A., Lee J., Gonzalez A., Chung M.,
Toriumi M., Chin C., Choi E., Chlou J., Gonzalez A., Chung M.,
Howng B., Koo T., Liu A., Vayaberg M., Altafi H., Brooks S.,
Buehler E., Chao Q., Con L., Conway A.B., Hansen N.,
Johnson-Hopson C., Khaf S., Kim C., Lam B., Nguyen M., Palm C.,
Shinn P., Davis R.W., Ecker J.R., Federspiel N.A., Theologis A.;
The sequence of BAC F2489 from Arabidopsis thaliana chromosome 1.";
Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 EGEEDTVAGSSIPKKKYMKQLTGKRDDTLLHSAVRHGNKDRVVEILTKTRESELNQLLGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QERVRKTSLDLRREII∯VGGIQN-----LIELRKKRKQKKRDALAASHEPPEPEEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     171 DNGATV-DFQDRLDCTAMHWACRGGHLEVVK-LLQSHGADTNVRDKLLSTPLHVAVRTGQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       229 VEIVEHFLSLG-LEINÄRDREGDTALHDAVRLNRYKIIKLLLLHG-ADMMTKNLAGKTPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ONOSGETALYVAAEYGDVEIVKEMINCYDLALVEI-----KARNGFDAFH-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ----AQSAALQKVKG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 543;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              287 DLVQLWQADTRHALEHPPE-----PGAEHNGLEGPNDSGRETPQPV 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                   databases
                                                                                                                                                                                                                                                                                                      EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C06C4C1B9E271DC8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21 EEENEKLRGDTRQKLPM-----DLLVLEDEKHHG-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 247.5; DB 1
Pred. No. 2.6e-09;
8; Mismatches 121
                                                                                                                                                                                                                                                                                                                                                                                                                   the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INCLUDES (JUN-2000) to the EMBL/GenBar Submitted (JUN-2000) to the EMBL/GenBar EMBL; AC007583; AAF75683.1; -. InterProx IPP00023; ank; 8 SWART; SW00248; ANK; 6 SWART; SW00248; ANK; 6 PROSITE; PS50299; ANK; 6 PROSITE; PS50299; ANK; 6 SEQUENCE 543 AA; 58911 MW; C06C4C1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-MAR-2001 (TYEMBLYEL. 16, Created)
01-MAR-2001 (TYEMBLYEL. 16, Last seq
01-JUN-2001 (TYEMBLYEL. 17, Last ann
TANKYRASE-LIKE PROTEIN (TANKYRASE 2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14.68;
29.18;
                                                                                                                                                                                                                                                                                                           the
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                                                                                                                                                                                                                                                                                                             <u>و</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity Matches 102; Conservati
                                                                                                                                                                                                                                                                                                                                                                                                    Theologis A.;
Submitted (DEC-1999)
                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
STRAIN=CV. COLUMBIA;
Theologis A.;
                                                                                                                                                                                                                                                                                                         Submitted (MAY-1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STEAIN-CV. COLUMBIA;
                                                                                                                                                                                                                                                                                                                                                                           STRAIN-CV. COLUMBIA;
                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SECUENCE FROM N.A
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14.6%; Score 247.5; DB 4
23.4%; Pred. No. 7.5e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE: PS50088; ANK_REPEAT; 15.
PROSITE: PS50297; ANK_REP_REGION; 1.
PROSITE: PS00190; CYTOCHROME_C; UNKNOWN_1.
NON_TER
1 1 SEQUENCE 1265 AA: 136405 MM.
                                                                                814 GVRSPGATADAL---SSGPSSPSSLSA 837
                                                      ----PGAEHNGLEGPNDSGRETPQPVPA 328
                                                                                                                                                                                                                                01-MAR-2001 (TrEMBLrel. 16, Created)
                                                                                                                                                                                         PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 23.4 Matches 105; Conservative
                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                             Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           856
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                                                        302
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Q9HAS4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                517 VNCRDIEGROSTPLHFAAGYNRVSVVEYLLQHGADVHAKDKGGLVPLHNACSYGHYEVAE 576
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ----STPLHVAVRTGQVEIVE 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          537 TDIQDLLRGDAALLDAAKKGCLARVKKLSSPDNVNCRDTQGRHSTPLHLAAGYNNLEVAE 696
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -- DTALHDAVRLN 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         : | | ::||:| ; | 697 YLLQHGADVNAQDKGGLIPLHNAASYGHVDVAALLIKYNACVNATDKWAFTPLHEAAQKG 756
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 80 GIQNLIELR-----KKRKQKKRDALA-ASHEPPPEFEEITGPVDEETFLK---- 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ---AAVEGKMKVIEKFLADGGSADTCDQFRRTALHRASLEGHMEILE 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RYKIIKLLLLHGADMMTKNLAGKTPTDLVQLWQADTRHAL-------EHPE--- 304
                                                                                                                                                                                                                                                                                                                                 novel
                                                                                                                                                                                                          "Cloning and characterization of TNKL, a member of tankyrase/ankyrin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         34 NEKLRGDTRQKLPMDLLVLEDEKHHGAQSAALQKVKGQERVRKTS----LDLRREIIDVG 79
                                                                                                                                                                                                                                                                                                                                                                                                                        Lyons R.J., Deane R., Lynch D.K., Ye Z.-S.J., Sanderson G.M., Eyre H.J., Sutherland G.R., Daly R.J.; "Identification of a novel human tankyrase through its interaction
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KLLDNGATVDFQDRLDCTAMHWACRGGHLEVVKLLQSHGA-------D
                Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
Kaminker P.G., Campisi J., Kim S.H., Yaswen P., Morin G.;
"Rapid induction of apoptosis by ectopic expression of TANK2, a
telomere-associated PARP.";
                                                                                                           SEQUENCE FROM N.A.
TISSUE-BREAST CARCINOMA;
Kuimov A.N., Kuprash D.V., Petrov V.N., Vdovichenko K.K.,
Boitchenko V.E., Scanlan M.J., Jongeneel C.V., Nedospasov S.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels 161;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 1166;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS50088; ANK_REPEAT; 15.
PROSITE; PS50297; ANK_REP_REGION; 1.
PROSITE; PS0190; CYTOCHROME_C; UNKNOWN_1.
SEQUENCE 1166 AA; 126917 WW; 4C8B3B8D97CEF704 CRC64;
                                                                                                                                                                                                                                                  Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                 Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 247.5; DB 4;
Pred. No. 6.7e-09;
9; Mismatches 133;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro: IPR002110; ANK.
InterPro: IPR000345; CytC_heme_bind.
InterPro: IPR001660; SAM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                with the adaptor protein Grb14.", J Blol. Chem. 0:0-012001)
EMBL; AF264912; AAG44694.1; -. EMBL; AF342982; AAK25811.1; -. EMBL; AF329696; AAK13463.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
14.6%;
Best Local Similarity 23.4%;
Matches 105; Conservative 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FRINTS; PRO1415; ANKYRIN.
SMART; SMO0248; ANK; 15.
SMART; SMO0454; SAM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00023; ank; 16.
Pfam; PF00536; SAM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HFLSLGLEINARDREG--
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                                                                                                                                                                                                                                                                                                                                                                                       [3]
SEQUENCE FROM N.A.
                                                                        NCBI_TaxID=9606;
                                                                                                                                                                                             Lagarkova M.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         168
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RYKIIKLLLLHGADMMTKNLAGKTPTDLVQLWQADTRHAL------EHPE--- 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24 NEKLRGDTRQKLPMDLLVLEDEKHHGAQSAALQKVKGQERVRKTS----LDLRREIIDVG 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          556 CDPNIISLOGFTALOMGNENVOOLLOEGISLGNSEADROLLEAAKAGDVETVKKLCTVOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TNVRDKLL-----STPLHVAVRTGQVEIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -----DTALHDAVRLN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               124 ------AAVEGKMKVIEKFLADGGSADTCDQFRRTALHRASLEGHMEILE
                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           161;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          80 GIQNLIELR------KKRKQKKRDALA-ASHEPPPEPEFITGPVDEETFLK---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 1265;
                                                                                                                                                                                                                      Moria D.W., Meses E.;
"Novel tankyrase-related gene.";
"Novel tankyrase-related gene.";
"Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AR305081; AAG25674.1; -.
InterPro; IPR000316; CytC_heme_bind.
InterPro; IPR000345; CytC_heme_bind.
InterPro; IPR000345; CytC_heme_bind.
Pfam; PF00023; ank; 16.
Pfam; PF00023; SAM: 1.
PRINTS; PR01415; ANKYRIN.
SMART; SM00248; ANK; 15.
SMART; SM00454; SAM: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3BFD7DE7AEBB0C38 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   168 KLLDNGATVDFQDRLDCTAMHWACRGGHLEVVKLLQSHGA-----
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
TANKYRASE-RELATED PROTEIN (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        49; Mismatches 133;
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10;
                                                                                                                                                                                                    138 -----ADGGSADTCDQFRRTALHRASLEGHMEILEKLLDNGATVDFQDRLDCTAMHWA 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            191 CRGGHLEVVKLLQSHGADTNVRDKLLSTPLHVAVRTGQVEIVEHFLSLGLEINARDREGD 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                       75 IIDVGGIQNLIELRKKRKQKKRDALAASHEPPPEPEEIT-------GPVDEET- 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                               24 NEKLRGDTROKLPMDLL-----VLEDEKHHGAQSAALQKVKGQERVRKTSLD--LRRE 74
                                                                                                                                    Homo sapiens (Human).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                             :06
                                                                                                                                                                                                                                                                                                                                                                        Query Match
14.4%; Score 244; DB 4; Length 1050;
Best Local Similarity 25.6%; Pred. No. 1e-08;
Matches 87; Conservative 46; Mismatches 117; Indels 9
                                                                            09H014;
01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-TUN-2001 (TrEMBLrel. 17, Last annotation update)
HYP: HETICAL 117.0 KDA PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TALHDAVRLNRYKIIKLLLLHGADMMTKNLAGKTPTDLVQ 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TALHEAVIEKHVFVVELLLIHGASVQVLNKRQRTAVDCAE 884
                                                                    PRT; 1050 AA.
305 ----PGAEHNGLEGPNDSGRETPQPVPA 328
             913 GVRSPGATADAL---SSGPSSPSSLSA 936
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -----FLKAAVEGKMKVIEKFL---
                                                                      PRELIMINARY;
                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                       Q9H0I4
                                                   RESULT 15
Q9H0I4
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Search completed: April 17, 2002, 08:13:56 Job time: 199 sec

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April 17, 2002, 08:09:42; Search time 23.95 Seconds (without alignments) 1017.541 Million cell updates/sec
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                  Compugen Ltd.
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GenCore version 4.5
Copyright (c) 1993 - 2000 Comp
                                                                                                                                                                                                                                                                                                                                522463 seqs, 74073290 residues
                                                                          - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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1693
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Sequence:
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

seq length: 0 seq length: 2000000000

Minimum DB Maximum DB

A\_Geneseq\_1101:\* Database :

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/SIDSB/ggddata/geneseqp/geneseqp/AA1991.DAT:\* Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

polypeptide polypeptide shear stress tankyrase. tankyrasel S SPANK. Homo tankyrase2 c polypeptide ORFX ORF2052 Human truncated ta Human tankyrase I Description Human Human Human Нишап Human Human Human Human Human SUMMARIES AAM42139 AAB90787 AAM40848 AAB42288 AAY44404 AAB27212 AAY44402 AAB66279 AAB47022 AAB66285 AAM40353 8 1327 1166 784 Query Match Length Score 892 658 296.5 282.5 249.5 249.5 249.5 249.5 249.5 Result ٠ ي

Human Grb7 effecto	rankyrase nomorodu	Human tankyrase II	Human tankyrase2 T	Human tankyrase2 r	Human tankyrase2 c	Tankyrase homologu	Human tankyrase2 c	Human tankyrase2 T	Human tankyrase2 c	Mouse SPANK. Mus	Human breast cance	н	O3	Arabidopsis thalla	U)	Human tankyrase2 c	Human death domain	Human polypeptide	Human polypeptide	Human protein kina	Drosophila tankyra	Human TRF1 TANK2 b	Human polypeptide	Human colon cancer	Human kidney ankyr	Human tankyrase II	2-5A-dependent RNA	Partial murine 2-5	Mouse 2-5A-depende	-5A-de	Fowlpox virus (FPV	virus pr	/ vecto
AAY05734	AA19//48	AAB27211	AAB66295	AAB66278	AAB66288	AAY97749	AAB66290	AAB66294	AAB66286	AAB47023	AAB48574	AAY72589	AAG41508	AAG41507	AAG41506	AAB66287	AAE01035	AAM38993	AAM39025	AAB85514	AAB66297	AAB66300	AAM39062	AAG75604	AAB62429	AAB27209	AAR59077	AAR82661	AAW12703	AAW94680	AAR58855	AAR58599	AAW10693
20	77	21	22	22	22	22	22	22	22	22	22	22	21	21	21	22	22	22	22	22	22	22	22	22	22	21	15	16	18	20	15	15	18
1074	1100	1166	1166	1169	1169	1240	1262	1385	756	991	907	1166	898	879	890	522	551	1715	1715	765	1181	362	840	705	1088	1333	619	619	619	619	422	422	422
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247.5		٠.	Ċ	ζ.	~	Ľ.	247.5	247.5	246.5	246	245.5	244	240.5	240.5	240.5	237.5	235	235	235	233	231	230.5	230.5	230	228	228	224	224	224	224	223	223	223
12	13	14	15	16	17	18	. 19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer; peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-brager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation; AAM40353 standard; Protein; 329 AA Human polypeptide SEQ ID NO 3498. 2000US-0552317. 2000US-0598042. 2000US-0620312. 2000US-0662191. 2000US-0662191. 2000US-062393. 26-DEC-2000; 2000WO-US34263 2000US-0488725 (first entry) WO200153312-A1. 25-APR-2000; 09-JUL-2000; 19-JUL-2000; 03-AUG-2000; 14-SEP-2000; 19-OCT-2000; 29-NOV-2000; Homo sapiens 21-JAN-2000; 22-0CT-2001 26-JUL-2001 leukaemia AAM40353; RESULT AAM40353 

Wang D;

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the invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAM38642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polynucleotides are useful immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral neuropathy and localised neuropathies and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression, Activinhibin activity, chemotactic/chemokinetic activity, hemocactic/chemokinetic activity, hemocactic/chemokinetic activity, arthritis and inflammation; leukaemias and
                                                                                                                                                                                                                                                                                                                                                                                C.N.S disorders.
Note: The sequence data for this patent did not form part of the printed
specification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RLDCTAMHWACRGGHLEVVKLLQSHGADTNVRDKLLSTPLHVAVRTGQVETVEHFLSLGL 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EINARDREGDTALHDAVRLNRYKIIKLLLHGADMMTKNLAGKTPTDLVQLWQADTRHAL 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121 FLKAAVEGKMKVIEKFLADGGSADTCDQFRRTALHRASLEGHMEILEKLLDNGATVDFQD 180
                                                                                                                   Novel nucleic acids and polypeptides, useful for treating disorders such as central nervous system injuries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MEDSEAVQRATALIEQRLAQEEENEKLRGDTRQKLPMDLLVLEDEKHHGAQSAALQKVKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QERVRKTSLDLRREIIDVGGIQNLIELRKKRKQKKRDALAASHEPPPEPEEITGPVDEET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ren F, W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 329;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                      Qian XB,
Yang Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 1688; DB 22;
Pred. No. 1.3e-155;
0; Mismatches 1;
                      Chen R, Ma Y, C
Xu C, Xue AJ,
R, Drmanac RT;
                                                                                                                                                                 Example 6; SEQ ID NO 3498; 10078pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EHPEPGAEHNGLEGPNDSGRETPQPVPAQ 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chen R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAM42139 standard; Protein; 182
                      Asundi V, Che
Wehrman T, Xu
Goodrich R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 99.7
Matches 328; Conservative
                                                                                WPI; 2001-442253/47.
                                                                                                                                                                                                                                                                                                                                                                                                                                               329 AA;
                                                     Zhou P,
(HYSE-) HYSEQ INC
                           Liu C,
Wang 2,
                                                                                              N-PSDB; AAI59509
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                              Tang
                                                         Zhao
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Gaps 9

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The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAM36642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polynucleotides are useful immunosuppressant and cytostatic activity. The polynucleotides are useful immunosuppressant and cytostatic activity. The polynucleotides of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral neuropathy and system, such as peripheral nervous injuries, peripheral neuropathy and alrheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression, activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, cancer diagnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The sequence data for this patent did not form part of the printed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 QERVRKTSLDLRREIIDVGGIQNLIELRKKRRQKKRDALAASHEPPPEPEEITGPVDEET 120
                                                                                                                                                                                                                                                                                                                                                                                                           Wang D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FLKAAVEGKMKVIEKFLADGGSADTCDQFRRTALHRASLEGHMEILEKLLDNGATVDFQ 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MEDSEAVQRATALIEQRLAQEEENEKLRGDTRQKLPMDLLVLEDEKHHGAQSAALQKVKG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    63
Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancel peripheral nervous system; cNS; Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-brager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  polypeptides, useful for treating disorders system injuries -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 892; DB 22; Length 182;
Pred. No. 1.1e-78;
0; Mismatches 1; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                Qian XB,
Yang Y,
                                                                                                                                                                                                                                                                                                                                                                                                            Chen R, Ma Y, (Xu C, Xue AJ, Drmanac RT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 2; SEQ ID NO 7070; 10078pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                Liu C, Asundi V, Chen R, Wang Z, Wehrman T, Xu C, Zhou P, Goodrich R, Drmana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  52.7%;
99.4%;
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19-JUL-2000; 2000US-059312.
03-AMG-2000; 2000US-0653450.
14-SEP-2000; 2000US-0662191.
19-OCT-2000; 2000US-0693036.
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2000US-0552317.
                                                                                                                                                                                                             26-DEC-2000; 2000WO-US34263
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         such as central nervous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2001-442253/47.
N-PSDB; AAI61295.
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Best Local Similarity
Matches 178; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       182 AA;
                                                                                                                                                                                                                                                                                                                                                                                       (HYSE-) HYSEQ INC.
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                                                                                                                                                     WO2 70153312-A1.
                                                                                                                                                                                                                                             21-JAN-2000; 2
25-APR-2000; 2
09-JUL-2000; 2
19-JUL-2000; 2
                                                                                                                        HOMO Sapiens.
                                                                                                                                                                                                                                                                                                                                                         29-NOV-2000;
                                                                                                                                                                                 26-JUL-2001.
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Wang J, W
Zhao QA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                          leukaemia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21
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AAB90787 standard; Protein; 319 AA.

AAB90787 RESULT

(first entry)

RESULT AAM40848

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The present invention provides the protein and coding sequences of a number of human shear stress response proteins. These are useful in the diagnosis, treatment and screening of vascular diseases caused by arteriosclerosis, including heart failure, post-PTCA restenosis and hypertension.
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                                                                                                                                                                                                                                                                            shear stress-response protein; vascular disease;
                                                                                                                                                                                 Human shear stress-response protein SEQ ID NO: 74.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 60; Page 425-427; 678pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (KYOW ) KYOWA HAKKO KOGYO KK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         02-OCT-2000; 2000WO-JP06840.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB; AAH02910.
                                                                                                                                                                                                                                                                                                                       arteriosclerosis
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                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-OCT-1999;
                                                                                          15-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12-APR-2001
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AAB90787;
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99JP-0280976.

Sakurada K;

Kawabata A,

M, Ota T, Sugano S;

Obayashi

Yoshisue H, Obayashi skine S, Nakamura Y,

Sekine S,

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5
                                                                                                                                                                                   109 PEEITGPVDEETFLKAAVEGKMKVIEKFLADGGSADTCDQFRRTALHRASLEGHMEILEK 168
                                                                                                                  LLDNGATVDFQDRLDCTAMHWACRGGHLEVVKLLQSHGADTNVRDKLLSTPLHVAVRTGQ 228
                                                                                                                                                        GAQSAALQKVKGQERVRKTSLDLRREIIDVGGIQNLIELRKKRKQKKRDALAASHEPPPE 108
                                               4,
                          Score 658; DB 22; Length 319;
Pred. No. 1.3e-55;
0; Mismatches 66; Indels 4
                                              50;
                          38.9%;
larity 51.8%;
Conservative 50
                                    Similarity
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319 AA;
                                              129;
                           Query Match
Best Local 3
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Matches
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Length 510; Indels

DB 22;

17.5%; Score 296.5; DB 22; 39.0%; Pred. No. 3e-20; 11ve 32; Mismatches 73;

69; Conservative

Matches

Ouery Match Best Local Similarity

510 AA;

Sequence

Note: The sequence data for this patent did not form part of the printed specification.

C.N.S disorders.

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The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAM38642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the Activity the activity chemotactic/chemokinetic activity, hemostatic and thrombolytic activity, chemotactic/chemokinetic activity, haemostatic and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Wang D;
                                                                                                                                                                                                                                                Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel nucleic acids and polypeptides, useful for treating disorders such as central nervous system injuries -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ren F, W
Zhang J;
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Yang Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  tu C, Xue AJ,
Drmanac RT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Xu C,
AAM40848 standard; Protein; 510 AA.
                                                                                                                                                                                     Human polypeptide SEQ ID NO 5779.
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Wehrman T, Xu
, Goodrich R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21-JAN-2000, 2000US-0488725.
25-APR-2000; 2000US-0552317.
09-JUL-2000, 2000US-0598042.
19-JUL-2000, 2000US-062312.
03-AUG-2000, 2000US-0653450.
14-SEP-2000, 2000US-0653191.
19-CCT-2000; 2000US-063313.
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                                                                                                                             (first entry)
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N-PSDB; AAI60004.
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Wang Z,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (HYSE-) HYSEQ INC.
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                                                                                                                          22-OCT-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                  leukaemia.
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Zhao QA,
                                                              AAM40848;
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(UYRQ ) UNIV ROCKEFELLER.
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                                                                                                                                                                                                                      Query Match
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Matches
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8×88888888888888
                                                                                                                                                                                                                                                                                                                  Human; open reading frame; ORFX; detection; cytostatic; hepatotropic; vulnerary; antipsoriatic; antiparkinsonian; nootropic; neuroprotective; anticonvulsant; osteopathic; antiarthritic; immunosuppessant; cardiant; anticonvulsant; thrombolytic; coagulant; vasotropic; antidabetic; immunosuppensive; dermatological; immunosuppessive; antiinflammatory; antiaviral; antibacterial; antifungul; antirheumatic; antithyroid; antiaviral; antibacterial; antifungul; antirheumatic; antithyroid; neurodegenerative disorder; osteoarthritis; graft vs host disease; cardiovascular disease; diabetes mellitus; hypothyroidism; scrib; Ancolesterol ester storage; systemic lupus erythematosus; infection; colesterol enmunodeficiency; malaria, autoimmune disorder; asthma; allery; aplastic anaemia; nocturnal haemoglobinuria; burn; wound; thrombogie; coagulation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                which represent the human ORFX open reading frames 1 to 3161. The ORFX which represent the human ORFX open reading frames 1 to 3161. The ORFX sequences have activities such as: cytostatic; hepatotropic; vulnerary; antipsoriatic; antiparkinsonian; nootropic; neuroprotective; osteopathic; anticonvulsant; antiarthritic; immunosuppressant; immunostimulant; cardiant; thrombolytic; coagulant; vasotropic; antidiabetic; hypotensive; dermatological; immunosuppressive; antiinflammatory; antibacterial; antiviral; antifungal; antirheumatic; antithyroid; and antianaemic. The sequences can be used for determining
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       to AAC77606 encode the proteins given in AAB40237 to AAB43397 vresent the human ORFX open reading frames 1 to 3161. The ORFX
                                                                       CTAMHWACRGGHLEVVKLLQSHGADTNVRDKLLSTPLHVAVRTGQVEIVEHFLSLGLEIN 243
  (24 AAVEGKMKVIEKFLADGGSADTCDQFRRTALHRASLEGHMEILEKLLDNGATVDFQDRLD 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         frame X,
                                                                                                              244 ARDREGDTALHDAVRLNRYKIIKLLLHGADMMTKNLAGKTPTDLVQLWQADTRHAL 300
                                                                                                                              Novel nucleic acids and peptides derived from open reading useful for treating e.g. cancers, proliferative disorders, neurodegenerative disorders and cardiovascular disease
                                                                                                                                                                                                                                                                                              SEQ ID NO:4104.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 11; Page 3289-3292; 5507pp; English.
                                                                                                                                                                                                                                                                                                  Human ORFX ORF2052 polypeptide sequence
                                                                                                                                                                                                                AAB42288 standard; Protein; 978 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99US-0127607.
99US-0127636.
99US-0127728.
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                                                                                                                                                                                                                                                                           08-FEB-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          thrombosis; contraceptive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Shimkets RA, Leach M;
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N-PSDB; AAC76497.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens.
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                                                                                                                                                                                                                                                   AAB42288;
                                                                   184
                                                                                                                                                                                                            AAB42286
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the presence of or predisposition to, or preventing or treating pathological conditions associated with an ORFX-associated disorder. The nucleic acids can be used to express ORFX proteins in gene therapy vectors. The proteins and nucleic acids may be used to treat cancers, proliferative disorders, neurodegenerative disorders, osteoarthritis, proliferation, hypothyroidsm, cholesterol ester storage, systemic lupus hypertension, hypothyroidsm, cholesterol ester storage, systemic lupus erythematosus, severe combined immunodeficiency (SCID), AIDS, viral, bacterial or fungal infection, malaria, autoimmune disorders, asthma, allergies, aplastic anaemia, burns, wounds, bone and cartilage damage, nocturnal haemoglobinuaia, antiinflammatory disease; to enhance coagulation; to inhibit thrombosis; and as a contraceptive.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human tankyrase; TRF1; telomeric repeat binding factor-1; telomere length regulation; recombinant tankyrase; aging; skin atrophy; macular degeneration; atherosclerosis; ataxia telangiectasia; tankyrase modulator; rational drug design.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            177 DFQDRLDCTAMHWACRGGHLEVVKLLQSHGADTNVRDKLLSTPLHVAVRTGQVEIVEHFL 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       392 lvdgidpnf---kmehqnkrsplhaaae-----aghvdichmlvqaganidtcsedq 440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         118 EETFLKAAVEGKMKVIEKFLADGGSADTCDQFRRTALHRASLEGHMEILEKLLDNG-ATV 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              347 ggpgketlesalialdsekpkklrfhpkqlyfsarggelqkvl-------lm 391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ---HHGAQSAALQKVKGQERVRKTSLDLRREII 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SLGLEINARDREGDTALHDAVRLNRYKIIKLLLLHGADMMTKNLAGKTPTDLV----QLW
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Pred. No. 1.7e-18;
1; Mismatches 120; Indels 77;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              77 DVGGIQNLIELRKKRKQKKRDALAASHEPPPEPEEITGPVD---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QA-DTRHALEHPEPGAEHNGLEGPNDSGRETPQPV 326
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98US-0196387.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human truncated tankyrase-2.
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28.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
                                                                                                                                                                                                                                                                                                                                                                    978 AA;
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17-AUG-1998;
19-NOV-1998;
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Human tankyrase; TRF1; telomeric repeat binding factor-1; two-hybrid screen; telomere length regulation; recombinant tankyrase; aging; skin atrophy; macular degeneration; atherosclerosis;
10-APR-2000; 2000WO-US09558
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                        09-APR-1999;
13-APR-1999;
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                                                                                                                                                                   length, ref
expression
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                                                                                        Morin GB,
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Best Local 3
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                                                                                                                                                The present sequence is truncated human tankyrase, a TRF1 (telomeric repeat binding factor-1) binding protein. This comprises 1-881 residues of human tankyrase. Tankyrase is involved in regulation of telomere length through TRF1 and may directly modulate the effect of TRF1 Recombinant tankyrase, or its fragments are used to identify specific modulators which are potential drugs for countering telomere shortening associated with adjing (e.g. atrophy of skin, macular degeneration or atherosclerosis) or diseases like ataxia telangiectasia. They are also used to raise specific antibodies (used as immunoassay reagents and as modulators of tankyrase activity) and in rational drug design.
                                                                           New nucleic acid encoding vertebrate tankyrase, a regulator of telomere length, used to identify modulators, e.g. for inhibiting growth of
                                                                                                                                                                                                                                                                                                                                                                                                                                  , 89 KKRKQ-----KKRDALAASHEPPPEPEEITGPVDEETFLKAAVEGKMKVIE 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                    135 KFLADGGSADTCDQFRRTALHRASLEGHMEILEKLLDNG------------------173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ----DRLDC-----TAMHWACRGG 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 636 qqilsestpirtsdvdyrlleaskaqdletvkqlcssqnvncrdlegrhstplhfaaqyn 695
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           484 ltyefkghsllqaareadlakvk----kt---laleiinfkqpqshetalhcavaslh 534
                                                                                                                                                                                                                                                                                                                                                            Indels 113; Gaps
                                                                                                                                                                                                                                                                                                                                                                                     LVLEDEKH---HGAQSAALQKVKGQERVRKTSLDLRREIIDVGGIQN-----LIELR 88
                                                                                                                                                                                                                                                                                                                                     DB 21; Length 949;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         tankyrase II; telomere length; signal transduction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            255 DAVRLNRYKIIKLLLHGADMMTKNLAGKTPTDLVQLWQADTRHALE 301
                                                                                                                                                                                                                                                                                                                                   ; Score 249.5; DB 21;
; Pred. No. 2.5e-15;
33; Mismatches 110;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human tankyrase I protein sequence SEQ ID NO: 8.
                                                                                                                           Disclosure; Page 125-129; 133pp; English.
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Local Similarity 26.2%;
les 91; Conservative 33
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              Smith S;
                                      WPI; 2000-116549/10.
                                                                                                                                                                                                                                                                                                949 AA;
                                                 N-PSDB; AAZ29633
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              Lange T,
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Best Local (
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The present sequence is a version of the human tankyrase I protein sequence. The invention relates to the isoaltion of the protein and coding sequences of human tankyrase II. This protein is thought to be involved in signal transduction in the cell, and to have binding activity for other telomere-associated proteins. It is possible that it plays a role in the regulation of telomere length, thus affecting the replicative ability of the cell. The protein is useful for ribosylating target proteins, for determining tankyrase II binding activity in a sample, and for modulating telomere length in a cell.
                                                                                                                                                                                                                                                                               Novel mammalian Tankyrase II polypeptide and the polynucleotide encoding the polypeptide useful for modulating or maintaining telomere length, replicative capacity, apoptosis, chromosome packing or gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      195 HLEVVKLLQSHGADTNVRDKLLSTPLHVAVRTGQVEIVEHFLSLGLEINARDREGDTALH 254
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            636 qqilsestpirtsdvdyrlleaskagdletvkqlcssqnvncrdlegrhstplhfaagyn
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26.2%; Pred. No. 4e-15;
iive 33; Mismatches 1
                                                                                                                                                            Piatyszek MA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 4; Fig 5; 52pp; English.
99US-0128577.
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                                                                                                                                                                                                                    WPI; 2000-679503/66.
                                                                                                                                                         Funk WD,
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                                                                                              (GERO-) GERON CORP.
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                                                                                                          //abbl=_Sterile_alpha_motif
1176..1314
/note= "Poly(ADP-ribose)polymerase (PARP) related domain'
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1023..1088
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                                                                                                                                                                                                                                                                                                                                                                                     New nucleic acid encoding vertebrate tankyrase, a regulator of teld
length, used to identify modulators, e.g. for inhibiting growth of
cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 1327;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  113;
ataxia telangiectasia; tankyrase modulator; rational drug design.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14.7%; Score 249.5; DB
26.2%; Pred. No. 4e-15;
.ive 33; Mismatches 1
                                                        Location/Qualifiers
181..1010
                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; Fig 1B; 133pp; English.
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98US-0135233.
98US-0196387.
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N-PSDB; AAZ29627.
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Best Local Similarity
Matches 91; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1327 AA;
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                                                                                                                                                                      WO9964606-A1
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                                    Homo sapiens
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                                                                                                                                                                                                                                                 10-JUN-1998;
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Domain
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The present invention provides the protein and coding sequence for the human tankyrase2 protein. This is found in two different versions, designated TANK2-LONG and TANK2-SHORT. Tankyrase2 has polyADP-ribosylation activity and is involved in the modification of TRFI, which is a telomere-specific binding protein. The regulation of telomere length, in which fRFI has a role, is linked to ageing and cancer. The sequences are useful in the treatment of cancers and inflammatory disorders.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    89 KKRKQ------KKRDALAASHEPPPEPEEITGPVDEETFLKAAVEGKMKVIE 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             484 ltyefkghsllqaareadlakvk-----kt---laleiinfkqpqshetalhcavasih 534
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New tankyrase2 polypeptides, useful for treating conditions mediated poly adenosine diphosphate-ribose) polymerase activity e.g. cancers, inflammatory and autoimmune disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         40 LVLEDEKH---HGAQSAALQKVKGQERVRKTSLDLRREIIDVGGIQN-----LIELR 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ---vaaerahndvme
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 1327;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        113;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     McElligott DL;
14.7%; Score 249.5; DB 22;
26.2%; Pred. No. 4e-15;
ive 33; Mismatches 110;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -----DRLDC--
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                                                                                                                                                                                                               AAB66279 standard; Protein; 1327
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Best Local Similarity 26.2
Matches 91; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; tankyrase2; TAN
inflammatory disorder.
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N-PSDB; AAF63838.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200100849-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         335
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AAB66285 standard; Protein; 784 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                     237 SLGLEINARDREG-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                inflammatory disorder
                                                                                                                                         1166 AA;
                                                                                                                                                                            Query Match
Best Local Similarity
Matches 93; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (ICOS-) ICOS CORP.
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                                                                                                                                           Sequence
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             HLEVVKLLQSHGADTNVRDKLLSTPLHVAVRTGQVEIVEHFLSLGLEINARDREGDTALH 254
                                                                                                                                                                                                                                      poly adenosine diphosphate-ribose polymerase; catalytic domain; ANK; ankyrin repeat; cytosol; insulin-responsive aminopeptidase; IRAP; GLUT4; adipocyte; insulin signalling pathway; hyperlipidaemia; glucose intolerance; atheromatous disease; atheroscierosis; obesity; cardiac insufficiency; coronary insufficiency; stroke; high blood pressure; non-insulin dependent diabetes; hypertension; hyperuricemia; Syndrome X; muscular dystrophy; muscle atrophy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (c) an ANK domain composed of ankyrin repeats.
SPANK is a cytosolic protein which can poly(ADP-ribosyl)ate itself.
SPANK binds insulin-responsive aminopeptidase (IRAP) and modulates
translocation of GLUT4 in the perinuclear region of adipocytes. It
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (a) a SAM (sterile alpha motif) domain;(b) a PARP (poly adenosine diphosphate-ribose polymerase) catalytic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The SPANK protein comprises
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New insulin signalling protein SPANK, useful for reducing body m
glucose intolerance or insulin resistance and for preventing or
treating obesity-related and muscle-related diseases
                                                                                                                                                                                                                                                                                                                                                                                         Misc-difference 375..362 "Encoded by nucleotides 1230..1337" Misc-difference 375..398
                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "Encoded by nucleotides 1695..1823"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  641..677
/note= "Encoded by nucleotides 2172..2282"
                                                                                                                                                                                                                             sterile alpha motif; PARP; insulin resistance;
                                              255 DAVRLNRYKIIKLLLHGADMMTKNLAGKTPTDLVQLWQADTRHALE 301
                                                         /note= "Encoded by nucleotides 768..878"
                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "Encoded by nucleotides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This sequence represents human SPANK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (WHED ) WHITEHEAD INST BIOMEDICAL RES. (GEHO ) GEN HOSPITAL CORP.
                                                                                                                             AAB47022 standard; Protein; 1166 AA.
                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
173..209
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                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                             ..524
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Misc-difference 482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chi N, Lodish HF;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200077225-A1.
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                                                                                                                                                                            29-MAR-2001
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                                                                                                                                                                                                     Human SPANK
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                                                                                                                                                    AAB47022;
                                                                                                                                                                                                                             SPANK;
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is an effector in the insulin signalling pathway in eukaryotic cells. SPANK is useful for reducing body mass, reducing glucose intolerance or insulin resistance, for preventing or treating obesity. related diseases or disorders, such as obesity, cardiac insufficiency, coronary insufficiency, stroke, hypertension atheromatous disease, atherosciencis, high blood pressure, non-insulin dependent diabetes, hyperlipideemia, hyperuricemia and Syndrome X and is also useful for preventing or treating muscle-related diseases or fatigue. Antibodies immunospecific for SPANK are useful for detecting the presence of SPANK polypeptide in a biological sample.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             236
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QSAALQKVKGQERVRKTSLDLRREIIDVGGIQNLIELRKKRKQKKRDALAASHEPPPEPE 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               qsvncrdlegqegislgnseadrqllea------akagdverqstpl 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             111 EITGPYDEETFLKAAVEGKMKVIEKFLADGGSADTCDQFRRTALHRASLEGHMEILEKLL 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   531 hf-----aagynrvsvveyllqhgadvhakdkgglvplhnacsyghyevaellv 579
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            264 IIKLLLLHGADMMTKNLAGKTPTDLVQLWQADTRHAL-------EHPE----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14.6%; Score 248; DB 22; Length 1166;
larity 24.2%; Pred. No. 4.7e-15;
Conservative 37; Mismatches 111; Indels 144;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human tankyrase2 clone protein sequence SEQ ID NO: 89.
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234 HFLSLGLEINARDREG--
           Homo sapiens
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                                                                                                                                                                                                                                                                                                         13;
                                                             mediated by cancers,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                195 livkhgavvnvadlwkftplheaaakgkyeickillqhgadptkknrdgntpldlvkdgd 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           nue present invention provides the protein and coding sequence for the human tankyrase2 protein. This is found in two different versions, designated TANK2-LONG and TANK2-SHORT. Tankyrase2 has modification of polyADP-ribosylation activity and is involved in the modification of TRPI, which is a telemere-specific binding protein. The regulation of telomene length, in which TRFI has a role, is linked to ageing and cancer. The sequences are useful in the treatment of cancers and inflammatory disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ---STPLHVAVRTGQVEIVE 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  tdiqdllrgdaalldaakkgclarvkklsspdnvncrdtqgrhstplhlaagynnlevae 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -----DTALHDAVRLN 260
                                                                                                                                                                                                                                                                                                                                                                                                                                 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                        194
                                                                                                                                                                                                                                                                                                                                                                                                        75 cdpniislqgftalqmgnenvqqllqegislgnseadrqlleaakagdvetvkklctvqs 134
                                                                                                                                                                                                                                                                                                                                24 NEKLRGDTRQKLPMDLLVLEDEKHHGAQSAALQKVKGQERVRKTS----LDLRREIIDVG 79
                                                                                                                                                                                                                                                                                                                                                   : | | ::||:|: | | | ||:| | yllqhgadvnaqdkyggliplhnaasyghvdvaallikynacvnatdkwaftplheaaqkg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          261 RYKIIKLLLLHGADMMTKNLAGKTPTDLVQLWQADTRHAL------EHPE---
                                                                                                                                                                                                                                                                                                                                                                                                                                                   --AAVECKMKVIEKFLADGGSADTCDQFRRTALHRASLEGHMEILE
                                                                                                                                                                                                                                                                                                                                                                                80 GIONLIELR-----KKRKQKKRDALA-ASHEPPPEPEEITGPVDEETFLK-----
                                                                                                                                                                                                                                                                                  DB 22; Length 784;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Grb7 effector; 2.2412 protein; human; signal transduction;
tumour marker; breast cancer; prostate cancer; prognosis;
                                                             New tankyrase2 polypeptides, useful for treating conditions poly(adenosine diphosphate-ribose) polymerase activity e.g. inflammatory and autoimmune disorders
                                                                                                                                                                                                                                                                                                             Indels
     McElligott DL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 168 KLLDNGATVDFQDRLDCTAMHWACRGGHLEVVKLLQSHGA----
                                                                                                                                                                                                                                                                                                             133;
                                                                                                                                                                                                                                                                                       Score 247.5; DB 2
Pred. No. 3.1e-15;
                                                                                                                                                                                                                                                                                      Query Match
14.6%; Score 247.5; I
Best Local Similarity 23.4%; Pred. No. 3.1e
Matches 105; Conservative 49; Mismatches
       Goldman PS,
                                                                                                                 Example 1; Page 144-146; 242pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            305 ----PGAEHNGLEGPNDSGRETPQPVPA 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HFLSLGLEINARDREG--------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAY05734 standard; Protein; 1074 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human Grb7 effector 2.2412 protein.
          Christenson E, Demaggio AJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
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                                 WPI; 2001-102896/11.
                                                                                                                                                                                                                                                                                                                                                                sekahnd-----
                                                                                                                                                                                                                                                        784 AA;
                                              N-PSDB; AAF63917
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19-JUL-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          diagnosis
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                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 12
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The present sequence represents a novel candidate effector for the Grb7 family of signalling proteins, termed 2.2412. The the Grb7 family of signalling proteins, termed 2.2412. The captence is predicted from a partial cDNA (see AAX25366). 2.2412 captured is predicted from a partial cDNA (see AAX25366). 2.2412 cmRNA transcripts (7 kb) were detected in all tissues examined containing a larger a muscle and placenta. Analysis of the sequence revealed skeletal muscle and placenta. Analysis of the sequence revealed significant homology to a large number of proteins containing conformation of the 2.2412 gene was localised to between chromosome 10q23.2 and proximal 10q23.32. Deletions in the chromosome 10q23.2 and proximal 10q23.32. Deletions in the chromosome logis. The 2.2412 gene was locationed the protein multiforme, melanoma and meningiomas. Detection of the protein multiforme, melanoma and meningiomas. Detection of the protein cancer and/or prognestic indicator for certain human cancers, in particular breast cancer and prostate cancer. Antagonism of the interaction between Grb7 family members and the canced protein should provide a novel treatment stategy for human diseases exhibiting aberrant receptor tyrosine kinase signalling, catch as cancer. Antiform a nibodies can be used in methods of cetecting the presence of 2.2412 protein in a sample.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           208
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -----AAVEGKMKVIEKFLADGGSADTCDQFRRTALHRASLEGHMEILE 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             425 vncrdiegrqstplhfaagynrvsvveyllghgadvhakdkgglvplhnacsyghyevae 484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New candidate effector*for the Grb7 family of signaling proteins, and specific antibody, juseful for detection and treatment of cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              168 KLLDNGATVDFQDRLDCTAMHWACRGGHLEVVKLLQSHGA-----D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    --STPLHVAVRTGQVEIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24 NEKLRGDTRQKLPMDLLVLEDEKHHGAQSAALQKVKGQERVRKTS----LDLRREIIDVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GIQNLIELR-----KKRKQKKRDALA-ASHEPPPEFEITGPVDEETFLK----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14.6%; Score 247.5; DB 20; 23.4%; Pred. No. 4.7e-15; ive 49; Mismatches 133;
                                                                                                                                                                                                                   (GAEV-) GARVAN INST MEDICAL RES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 9; Fig 1; 24pp; Énglish.
                                                                                                                                                              97AU-0009388.
                                                                                                   98WO-AU00795
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Best Local Similarity 23.4%
Matches 105; Conservative
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                                                                                                                                                                                                                                                                                 Daly RJ, Sutherland
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N-PSDB; AAX25366.
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                                                                                                            23-SEP-1998;
                                                                                                                                                                    23-SEP-1997;
W09915647-A1
                                                    01-APR-1999
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233

--STPLHVAVRTGQVEIVE

AAY97748;

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AAY97748

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391 cdpniislggftalgmgnenvggllgegislgnseadrglleaakagdvetvkklctvgs 450
                                                                                                                                                   -------AAVEGKMKVIEKFLADGGSADTCDQFRRTALHRASLEGHMEILE
                                                                                                                                                                                           vncrdiegrqstplhfaagynrvsvveyllqhgadvhakdkgglvplhnacsyghyevae
                                                                                                                                                                                                                                    168 KLLDNGATVDFQDRLDCTAMHWACRGGHLEVVKLLQSHGA-------D
                                                                                                                                                                                                                                                                                                                                                               571 tdiqdllrgdaalldaakkgclarvkklsspdnvncrdtggrhstplhlaagynnlevae
                                                                                                                                                                                                                                                                                                                                                                                                            234 HFLSLGLEINARDREG-----DTALHDAVRLN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              261 RYKIIKLLLLHGADMMTKNLAGKTPTDLVQLWQADTRHAL-------EHPE---
                                                                GIQNLIELR-----KKRKQKKRDALA-ASHEPPPEPERITGPVDEETFLK----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; tankyrase II; telomere length; signal transduction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human tankyrase II protein sequence SEQ ID NO: 6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          note- "encoded by TTA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note= "encoded by TAC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ---- PGAEHNGLEGPNDSGRETPQPVPA 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          748 gvrspgatadal----ssgpsspsslsa 771
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Piatyszek MA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAB27211 standard; Protein; 1166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10-APR-2000; 2000WO-US09558
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99US-0129123
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N-PSDB; AAC66825.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Misc-difference 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Misc-difference 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (GERO-) GERON CORP.
                                                                                                                                                                                                                                                                                                                         TNVRDKLL----
                      342 sekahnd----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
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13-APR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This sequence is the Tankyrase homologue isotype I (TaHo-1) protein of the invention. The invention also relates to the TaHo-2 protein. The TaHo proteins are useful for inducing or preventing cell proliferation in cells, and in the study or treatment of conditions mediated by the cell cycle proteins, such as to diagnose, treat or prevent cell cycle associated disorders, preferably cancer. The TaHo coding sequences are useful as hybridisation probes, in chromosome and gene mapping and in the generation of anti-sense DNA and RNA. The coding sequences are also useful for the preparation of TaHo, for generating either transgenic animals or knock out animals which, in turn, are useful in a development and screening of therapeutically useful agents, in gene threapy, as vaccine, and for construction of hybridisation probes for mapping the gene which encodes TaHo and for the genetic analysis of individuals with genetic disorders. The TaHO proteins, and their coding
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tankyrase homologue isotype 1; TaHO-1; TaHO-2; cell proliferation; cell cycle protein; cell cycle associated disorder; cancer; gene mapping; chromosome mapping; gene therapy; vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel recombinant cell cycle polypeptide, tankyrase H useful for inducing or preventing cell proliferation in cells, and for diagnosing, treating or preventing cell cycle associated disorders such as cancer
                                                                     | :: ||| ||| || || || || || || || || rtqlcalllahgadptlknqegqtpldlv---saddvsalltaamppsalpscykpqvln 721
605 yllqhgadvnaqdkggliplhnaasyghvdvaallikynaslnatdkwaftplheaaqkg 664
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                            Tankyrase homologue isotype 1 protein sequence.
                                              RYKIIKLLLLHGADMMTKNLAGKTPTDLVQLWQADTRHAL-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sequences are useful in screening assays.
                                                                                                                               ----PGAEHNGLEGPNDSGRETPQPVPA 328
                                                                                                                                                                       722 gvrspgatadal----ssgpsspsslsa 745
                                                                                                                                                                                                                                                                              AAY97748 standard; Protein; 1100 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Huang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25-OCT-2000; 2000WO-US41528.
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                                                                                                                                                                                                                                                                                                                                                                   (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chan E, Xu X,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unidentified.
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Luo Y,

Novel mammalian Tankyrase II polypeptide and the polynucleotide encoding the polypeptide useful for modulating or maintaining telomere length, replicative capacity, apoptosis, chromosome packing or gene expression

24 NEKLRGDTROKLPMDLLVLEDEKHHGAQSAALQKVKGQERVRKTS----LDLRREIIDVG 79

Segmence

Query Match

Best Loca Matches

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DĽ;

McElligott

Goldman PS,

Demaggio AJ,

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2001-102896/11
     (ICOS-) ICOS CORP
                                                             N-PSDB; AAF63953
                             Christenson E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 637
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13;
                 The present sequence is a version of the human tankyrase II protein sequence. The protein is thought to be involved in signal transduction in the cell, and to have binding activity for other telomere-associated proteins. It is possible that it plays a role in the regulation of telomere length, thus affecting the replicative ability of the cell. The protein is useful for ribosylating target proteins, for determining tankyrase II binding activity in a sample, and for modulating telomere length in a cell.
                                                                                                                                                                                                                                                                                                                                                                                                                                             697 yliqhgadvnaqdkggliplhnaasyghvdvaallikynacvnatdkwaftpiheaaqkg 756
                                                                                                                                                                                                                                                                                                                                                          989
                                                                                                                                                                                                                                                                                                              517 vncrdiegrqstplhfaagynrvsvveyllqhgadvhakdkgglvplhnacsyghyevae 576
                                                                                                                                                                                                                                                                                                                                                                              ----STPLHVAVRTGQVEIVE 233
                                                                                                                                                                                                                                                                                                                                                                                                                          --- DTALHDAVRLN 260
                                                                                                                                                                                                                      ----vvevvvkheakvnaldnl-gqtslhraaycghlqtcrlllsyg 456
                                                                                                                                                                                                                                           80 GIQNLIELR-----KKRKQKKRDALA-ASHEPPPEPEEITGPVDEETFLK----- 123
                                                                                                                                                                                                                                                                                         AAVEGKMKVIEKFLADGGSADTCDQFRRTALHRASLEGHMEILE 167
                                                                                                                                                                              Indels 161; Gaps
                                                                                                                                                                                                 24 NEKLRGDTRQKLPMDLLVLEDEKHHGAQSAALQKVKGQERVRKTS----LDLRREIIDVG 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; tankyrase2; TANK2; TRF1; telomere; cancer; neoplasm; aging;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ||:::| |
tdiqdllrgdaalldaakgclarvkklsspdnvncrdtggrhstplhlaagynnlevae
                                                                                                                                                                                                                                                          ---EHPE---
                                                                                                                                                        DB 21; Length 1166;
                                                                                                                                                          ; Score 247.5; DB 21;
; Pred. No. 5.3e-15;
49; Mismatches 133;
                                                                                                                                                                                                                                                                                                                                       KLLDNGATVDFQDRLDCTAMHWACRGGHLEVVKLLQSHGA-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RYKIIKLLLLHGADMMTKNLAGKTPTDLVQLWQADTRHAL-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human tankyrase2 TANK2-SHORT SEQ ID NO: 135.
                                                                                                                                                                                                                                                                                                                                                                                                                                HFLSLGLEINARDREG-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ||| : | : | : |
gvrspgatadal----ssgpsspsslsa 837
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ---- PGAEHNGLEGPNDSGRETPQPVPA 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ä.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAB66295 standard; Protein; 1166
   Claim 4; Fig 4; 52pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28-JUN-2000; 2000WO-US17827
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99US-0141582
                                                                                                                                                           14.68; 23.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                     TNVRDKLL------
                                                                                                                                                                                 Matches 105; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 inflammatory disorder
                                                                                                                            1166 AA;
                                                                                                                                                                        Similarity
                                                                                                                                                                                                                             408 sekahnd----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAB66295;
                                                                                                                             Sequence
                                                                                                                                                             Query Match
Best Local $
                                                                                                                                                                                                                                                                                                                                                                                                                                234
                                                                                                                                                                                                                                                                                              124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAB66295
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention provides the protein and coding sequence for the human tankyrase2 protein. This is found in two different versions, designated TANK2-ENORG and TANK2-SHORT. Tankyrase2 has polyADP-ribosylation activity and is involved in the modification of TRF1, which is a telomere-specific binding protein. The regulation of telomere length, in which TRF1 has a role, is linked to ageing and cancer. The sequences are useful in the treatment of cancers and inflammatory disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ----- 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New tankyrase2 polypeptides, useful for treating conditions mediated poly(adenosine diphosphate-ribose) polymerase activity e.g. cancers, inflammatory and autoimmune disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NEKLRGDTRQKLPMDLLVLEDEKHHGAQSAALQKVKGQERVRKTS----LDLRREIIDVG 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -AAVEGKMKVIEKFLADGGSADTCDQFRRTALHRASLEGHMEILE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 vncrdiegrqstplhfaagynrvsvveyilqhgadvhakdkgglvplhnacsyghyevae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          tdiqdilrgdaalldaakkgclarvkklsspdnvncrdtggrhstplhlaagynnlevae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cdpniislqgftalqmgnenvqqllqegislgnseadrqlleaakagdvetvkklctvqs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GIQNLIELR-----KKRKQKKRDALA-ASHEPPPEPEEITGPVDEETFLK-----
                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 1166;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels 161;
                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 22;
                                                                                                                                                                                                                                                                                                                                                                                                                          14.68; Score 247.5; DB 22; 23.48; Pred. No. 5.3e-15; wiematches 133;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RYKIIKLLLHGADMMTKNLAGKTPTDLVQLWQADTRHAL---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KLLDNGATVDFQDRLDCTAMHWACRGGHLEVVKLLQSHGA-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              completed: April 17, 2002, 08:10:16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ----PGAEHNGLEGPNDSGRETPOPVPA 328
                                                                                                     Claim 3; Page 200-203; 242pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TNVRDKLL------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HFLSLGLEINARDREG-
                                                                                                                                                                                                                                                                                                                                                                          1166 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 105; Conserv
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Job time: 34 sec
                                                                                                                                                                                                                                                                                                                                                                            Sequence
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OLASIN ARMA HABAR SIHLA

(OTABU) MALE BLANK (USPTO)

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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- protein search, using sw model OM protein April 17, 2002, 08:09:42; Search time 16.03 Seconds Run on:

(without alignments)
1563.408 Million cell updates/sec

US-09-758-593A-1 Title:

Perfect score:

1693 1 MEDSEAVQRATALIEQRLAQ......NGLEGPNDSGRETPQPVPAQ Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 oring table:

219241 segs, 76174552 residues Searched: Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR\_68:\* Database :

pirl:\* pir2:\* pir3:\* pir4:\*

3. ..

## SUMMARIES

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	cytokine inducible	hypothetical prote	ankyrin - fruit fl	probable ankyrin [	hypothetical prote		٦,		7,	ankyrin, erythrocy	,	'n	m	'n	'n	m	ed	Ω,	hypothetical prote	_	G9a protein - huma	inversin - mouse	Inv protein - mous	ankyrin-related pr	hypothetical prote	н	ankyrin-related un	ankyrin-related un	2-5A-dependent RNA
	ID	72	C86212	T13940	D84448	T43458	B35049	A35049	SJHUK	S37431	S37771	149502	T42714	T42715	T42713	T42716	A55575	151192	T17278	E86190	B45771	830385	T30255	T14151	A57282	T21884	T15346	S	34	A45771
	DB	7	7	7	~	7	~	~	-	• •		~	7	•	7	•	~	•	~	~						~				
	Match Length	319	543	1549	247	1031	1856	1880	1881	3924	1848	1862	1765	1940	1943	1961	4377	318	641	627	619	1001	1062	1062	1786	1398	1815	1867	2039	741
a Ouerv	Match	38.9		14.1		13.9		13.9		٠.							13.5		m.			13.2		13.1		12.9				12.8
	Score	658	247.5	238.5	237.5	235	234.5	234.5	234.5	234.5	233.5	233.5	230	230	230	230	229	228.5	228	226	224	223.5	222.5	222	221	218	218	218	218	217
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hypothetical prote hypothetical prote	ankyrin-like repea ankyrin-like prote	ankyrin-like prote hypothetical prote	sex-determining pr GA-binding protein	GA-binding protein nuclear respirator	nuclear respirator nuclear respirator	nuclear respirator ankyrin related pr	death-associated p hypothetical prote
T24158 T24157	B47169 E84725	T48283 G84427	A34793 C40858	B40858 C48146	I38744 I38743	I38741 T19006	I37275 T46445
0.0	7 7	77	0 0	7 7	7 7	77	7
2584	323 662	517 532	656 347	382	348 360	395 1016	1423 397
12.8	12.7	12.6 12.5	12.5 12.3	12.3 12.3	12.3	12.2	12.0 11.9
216 216	215 214.5	$213.5 \\ 212$	212 208.5	208.5	207.5	206.5	203.5 201
30 31	32 33	34 35	36 37	38 30 8	40	4243	44 45

## ALIGNMENTS

```
C; Species: Homo sapiens (man)
C;Date: 01-Dec-1995 #sequence_revision 01-Dec-1995 #text_change 20-Sep-1999
C;Accession: A51291; S54205
R;Chu, W.; Burns, D.K.; Swerlick, R.A.; Presky, D.H.
B. Biol. Chem. 270, 10336-10244, 1995
A;Title: Identification and characterization of a novel cytokine-inducible nuclear pr
A;Reference number: A57291; MUID:95247734
                                                                                                                                                                                                                                                                                                                        A; Accession: A57291
A; Status: preliminary
A; Molecule type: mRNA
A; Residues: 1-319 <CHU>
A; CHU>
A; CHU>
C; Superfemees: EMBL: X83703; NID: 9793840; PIDN: CAA58676.1; PID: 9793841
C; Superfemily: unassigned ankyrin repeat proteins; ankyrin repeat homology; EGF homol C; Keywords: nucleus
protein C193 - human
cytokine inducible nuclear
```

7 Gaps 4. Length 319 66; Indels 38.9%; Score 658; DB 2; 51.8%; Pred. No. 6.9e-38; ive 50; Mismatches 66 Query Match 38.9 Best Local Similarity 51.8 Matches 129; Conservative

GAQSAALQKVKGQERVRKTSLDLRREIIDVGGIQNLIELRKKRKQKKRDALAASHEPPPE 108 PEEITGPVDEETFLKAAVEGKMKVIEKFLADGGSADTCDQFRRTALHRASLEGHMEILEK 168 LLDNGATVDFQDRLDCTAMHWACRGGHLEVVKLLQSHGADTNVRDKLLSTPLHVAVRTGQ 228 229 VEIVEHFLSLGLEINARDREGDTALHDAVRLNRYKIIKLLLLHGADMMTKNLAGKTPTDL 288 112 49 109 169 q g g à δ

232 YECAEHLIACEADLNAKDREGDTPLHDAVRLNRYKMIRLLIMYGADLNIKNCAGKTPMDL 291 qq ŏ

289 VQLWQADTR 297 a à

RESULT C86212

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hypothetical protein [imported] - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Species: 0.2 Mar-2001 #sequence\_revision 0.2 Mar-2001 #text\_change 31-Mar-2001
C;Accession: C86212
C;Accession: C86212
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alon Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar,

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probable ankyrin (imported) - Arabidopsis thaliana (c.Species: Arabidopsis thaliana (mouse-ear cress) (c.Species: Arabidopsis thaliana (mouse-ear cress) (c.Species: Data (c.Species: Data) (c.S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana. A; Reference number: A84420; MUID:20083487
A; Accession: D84448
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-247 <STO>
A; Cross-references: GB:AE002093; NID:g4335756; PIDN:AADI7433.1; GSPDB:GN00139
C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hypothetical protein DKF2p434F0621.1 - human hypothetical protein DKF2p434F0621.1 - human c;Species: Homo sapiens (man) c;Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 21-Jan-2000 C;Accession: T43458 R;Blum, H.; Bauersachs, S.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S. submitted to the Protein Sequence Database, December 1999 A;Reference number: 222517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GATVDFQDRLDCTAMHWACRGGHLEVVKLLQSHGADTNVRDKLLSTPLHVAVRTGQVEIV 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DEETFLKAAVECKMKVIEKFLADGGSADTC----DQFRRTALHRASLEGHMEILEKLLDN 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              46 DGRSLLHVAASFGHSQIVKLLSSSDEAKTVINSKDDEGWAPLHSAASIGNAELVEVLLTR 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             668 LAAQGGNVDMVQLLLEYGV-ISAAAKNGLTPLHVAAQEGHVLVSQILLEHGANISERTRN 726
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 | : | || : | || : | || :| || :| || EFLIEEGAEIDATDKNGQTALMHSVICDDKQLKVSMDQYAFLLIRHGADVDVEDKEGYT 224
                    75 IIDVGGIQNLIELRKKRKQKKRDALAASHEPPPEPEEITGPVDEETFLKAAVEGKMKVIE
                                                                                                                                                                                                                                                                                                                                                                                                            222 VAVRICQVEIVEHFLSLGLEINARDREGDTALHDAVRLNRYKIIKLLLLHGADMMTKNLA
                                                                                                                                               135 KFLADGGSADTCDQFRRTALHRASLEGHMEILEKLLDNGATVDFQDRLDCT-----
                                                                                                                                                                                                      548 VLLENGAENNAVTKKGFTPLHLACKYGKQNVVQILLQNGASIDFQGKNDVTPLHVATHYN
                                                                                                                                                                                                                                                                                                                   608 NPSIVELLLKNGSSPNLCARNGQCAIHIACKKNYLEIAMQLLQHGADVNIISKSGFSPLH
                                                                                  ----IAAKEGQENIVQ
                                                                                                                                                                                                                                                                                 ----AMHWACRGGHLEVVKLLQSHGADTNVRDKLLSTPLH
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                                                                    SO7 LGNINIIMLLLQHGAEINAQSNDKYSALH----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              727 GYTPLHMAAHYGHLDLVKFF 746
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     282 GKTP-----TDLVQLW 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 34.1'
Matches 61; Conservative
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A;Status: preliminary
A;Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Map position: 2
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Subreuil, R.R.; Yu, J.
A; Title: Ankyrin and beta-spectrin accumulate independently of alpha-spectrin in Drosoph A; Reference number: 217820; MUID:95024098
A; Reference number: 217820; MUID:95024098
A; Recession: T19940
A; Recule type: DNA
A; Residues: 1-1549 CDUB>
ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
Asturer 408, 816-820, 2000
Asturer 408, 816-820, 2000
C.; Khan, S.; Khaykin, E.; Kim, C.
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Roney, T.; Rowley, D.; Sakano, H.
A.Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A.; File: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9
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                                                                                                                                                                                                                                                                              A; Accession: C86212
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-543 <STO>
A; Cross references: GB: AE005172; NID: 98439897; PIDN: AAF75083.1; GSPDB: GN00141
C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Species: Drosophila melanogaster
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 17-Nov-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A,Cross-references: EMBL:L35601; NID:9557083; PID:9557084; PIDN:AAC37208.1
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VEIVEHFLSLG-LEINARDREGDTALHDAVRLNRYKIIKLLLLHG-ADMMTKNLAGKTPT 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             62 QNQSGETALYVAAEYGDVEIVKEMINCYDLALVEI-----RARNGFDAFH------ 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      113 TGPVDEETFLKAAVEGKMKVIEKFLADGGS--ADTCDQFRRTALHRASLEGHMEILEKLL 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 QERVRKTSLDLRREIIDVGGIQN-----LIELRKKRKQKKRDALAASHEPPPEPEI 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 EGEEDTVAGSSIPKKKMMKQLTGKRDDTLLHSAVRHGNKDRVVEILTKTRESELNQLLGK 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ---AQSAALQKVKG- 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -----IAAKQGDLDVL-KVLAEAHSELAMTVDLSNTTALHTAATQGHTEVVNFLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          : |:::
ELGSSLAGIAKSNGRTALHSASRNGHVKVIKALLASEPAIAIRMDKKGQTALHMAVKGTN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            171 DNGATV-DFQDRLDCTAMHWACRGGHLEVVK-LLQSHGADTNVRDKLLSTPLHVAVRTGQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  69;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               79;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DLVQLWQADTRHALEHPE-----PGAEHNGLEGPNDSGRETPQPV 326
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Best Local Similarity 25.0%; Pred. No. 2.2e-08;
Matches 80; Conservative 51; Mismatches 120;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 247.5; DB 2
Pred. No. 1.4e-09;
3; Mismatches 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21 EEENEKLRGDTRQKLPM------DLLVLEDEKHHG-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14.6%;
29.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         102;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local S:
Matches 102,
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Length 1856; Indels

DB 2;

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13.9%; Score 234.5; DB 2
33.5%; Pred. No. 5.1e-08;
ive 29; Mismatches 87
F;733-765/Domain: ankyrin repeat homology <AN22>F;766-798/Domain: ankyrin repeat homology <AN23>
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33.5%;
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                                                                                                                                                                            Query Match 13.99
Best Local Similarity 33.59
Matches 60; Conservative
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Best Local Similarity
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R; Lambert, S; Yu, H; Prchal, J.T.; Lawler, J.; Ruff, P.; Speicher, D.; Cheung, M.C.; Proc. Natl. Acad. Sci. Us.A. 87, 1730-1734, 1990
A; Title: cDNA sequence for human erythrocyte ankyrin.
A; Reference number: A35049; MUID: 90175370
A; Accession: B35049
A; Status: preliminary
B; Molecule type: mRNA
Residues: 1-1856 < LAM>
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F:2-1513,1676-1856/Product: ankyrin 2.2, erythrocyte #status predicted <MA2>
F:44-76/Domain: ankyrin repeat homology <AN01>
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N;Alternate names: ankyrin 2.1, erythrocyte; ankyrin-R
N;Contains: ankyrin 2.2, erythrocyte
C;Species: Homo sapiens (man)
C;Species: Howo-1995 #sequence_revision 17-Nov-1995 #text_change 10-Jul-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         116 VDEE-----TFLKAAVE-GKMKVIEKFLADGGSADTCDQFRRTALHRASLEGHMEILEKL 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ---GAD 208
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                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                              42;
                                                                                                                                                                                                                                                                                                                           13.9%; Score 235; DB 2; Length 1031; 33.5%; Pred. No. 2.3e-08; ive 33; Mismatches 68; Indels 4
                                            A;Cross-references: EMBL:ALl33620
A;Experimental source: adult testis; clone DKF2p434F0621
C;Genetics:
A;Note: DKF2p434F0621.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         257 VRLNRYKIIKLLLLHGAD----MMTKNLAGKTPTDL 288
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A,Cross-references: GDB.118737; OMIM:182900
A;Map position: 8p11.2-8p11.2
C,Superfamily: ankyrin; ankyrin repeat homology
C,Keywords: alternative splicing
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F;238-270/Domain: ankyrin repeat
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F;535-567/Domain: ankyrin repeat
F;568-600/Domain: ankyrin repeat
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Rilambert, S.; Yu, H.; Prchal, J.T.; Lawler, J.; Ruff, P.; Speicher, D.; Cheung, M.C. Proc. Natl. Acad. Sci. U.S.A. 87, 1730-1734, 1990
A;Title: cDNA sequence for human erythrocyte ankyrin.
A;Reference number: A35049; MUID:90175370
A;Reference number: A35049
A;Status: preliminary
A;Wolecule type: mRNA
A;Residues: 1-1880 < LAM>A;Cross_references: GB:M28880
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Gene: GDB:ANK1; ANK
A;CROSs-references: GDB:118737; OMIM:182900
A;CROSs-references: GDB:11.2-8p11.2
C;Superfamily: ankyrin; ankyrin repeat homology
C;Seywords: alternative splicing; cytoskeleton
E;2-1880/Product: ankyrin 1, erythrocyte form 2 #status predicted <MMI>P;2-1513,1676-1880/Product: ankyrin 2.2, erythrocyte #status predicted <MMI>
                                                                                                                                                                                                                                                                                                                                                             ankyrin 1, erythrocyte splice form 2 - human
N:Alternate names: ankyrin 2.1, erythrocyte; ankyrin-R
N;Contains: ankyrin 2.2, erythrocyte
C;Species: Homo sapiens (man)
C;Date: 27.-Jul-1990 #sequence_revision 01-Oct-1992 #text_change 04-Sep-1998
C;Accession: A35049
108 EPEEITGPVDEETFLKAAVEGKMKVIEKFLADGGSADTCDQFRR-TALHRASLEGHMEIL 166
                              | ::|| :| | | | : |: :: | | | 330 EIDDIT--LDHLTPLHVAAHCGHRVAKVLLDKGAKPNSRALNGFTPLHIACKKNHVRVM 387
                                                                                             EKLLDNGATVDFQDRLDCTAMHWACRGGHLEVVKLLQSHGADTNVRDKLLSTPLHVAVRT 226
                                                                                                                      227 GQVEIVEHFLSLGLEINARDREGDTALHDAVRLNRYKIIKLLLLHGADMMTKNLAGKTP 285
                                                                                                                                                                                                                    Length 1880;
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Pred. No. 5.2e-08;
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submitted to the EMBL Data Library, September 1993
A;Reference number: $37431
A;Reference number: $37431
A;Reference number: $37431
A;Reference relation and A;Residues: 1-394 <CHA>
A;Reference number: Reference number: A39643; MUID:91302466
A;Reference number: A39643; MUID:91302466
A;Accession: A39643
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A; Residues: 463-474, 'PE', 477-495 <TSE>
A; Cross-references: GB:M31123; NID:9178647; PIDN:AAA62828.1; PID:9178648
R; Chan, W.; Kordeli, E.; Bennett, V.
J. Cell Biol. 123, 1463-1473, 1993
A; Title: 440-kb ankyrinB: structure of the major developmentally regulated domain and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ankyrin 2, neuronal long splice form - human N;Alternate names: ankyrin B, 440K splice form; ankyrin-B; brain ankyrin; non-erythro N;Contains: ankyrin 2, short form C;Species: Homo sapiens (man) C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 13-Aug-1999 C;Accession: S37431; A39643; B39643; A40334; A40462; S14533; S14569
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A; Residues: 1-1443,3585-3924 <OTT>
A; Cross-references: EMBL:X56958
F; Tse, W.T.; Menninger, J.C.; Yang-Feng, T.L.; Francke, U.; Sahr, K.E.; Lux, S.E.; Wa
Genomics 10, 858-866, 1991
A;Title: Isolation and chromosomal localization of a novel nonerythroid ankyrin gene.
A;Reference number: A40334; MUID:92009921
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EPEEITGPYDEETFLKAAVECKMKVIEKFLADGGSADTCDQFRR-TALHRASLEGHMEIL 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     167 EKLLDNGATVDFQDRLDCTAMHWACRGGHLEVVKLLQSHGADTNVRDKLLSTPLHVAVRT 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 330 EIDDIT--LDHLIPLHVAAHCGHHRVAKVLLDKGAKPNSRALNGFIPLHIACKKNHVRVM 387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GQVEIVEHFLSLGLEINARDREGDTALHDAVRLNRYKIIKLLLLHGADMMTKNLAGKTP 285
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              F;502-534/Domain: ankyrin repeat homology <ANI5>
F;585-607/Domain: ankyrin repeat homology <ANI5>
F;586-600/Domain: ankyrin repeat homology <ANI6>
F;601-633/Domain: ankyrin repeat homology <ANI8>
F;601-633/Domain: ankyrin repeat homology <ANI8>
F;607-699/Domain: ankyrin repeat homology <ANI9>
F;607-699/Domain: ankyrin repeat homology <ANI9>
F;700-732/Domain: ankyrin repeat homology <AN20>
F;766-798/Domain: ankyrin repeat homology <AN20>
F;766-798/Domain: ankyrin repeat homology <AN21>
F;766-798/Domain: ankyrin repeat homology <AN23>
F;868-1382/Domain: 62K #status predicted <DOM2>
                                                                                                                                                                                                                                 <AN21>
                                                                                                                           <AN18>
                                                                                                                                                                                                    <AN20>
                                                                                                                                                                                                                                                                                                       <AN23>
                                                                                                                                                                                                                                                                                                                                                                                                         F;1383-1881/Domain: 55K #status predicted <DOM3>
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ankyrin repeat
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A;Molecule type: mRNA
A;Residues: 1-2077 < OTL>
A;Cross-references: GB:X56957
A;Accession: B39643
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Best Local Simi
Matches 60;
   F;469-501/Domain:
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A; Residues: 1-1881 <LU1>
A; Accession: A3229
A; Accession: A3229
A; Molecule type: protein
A; Note: 845-Arg and 1392-Thr were also found
R; Hermann, J; Barel, M; Frade, R.
A; Note: 845-Arg and 1392-Thr were also found
R; Hermann, D; Barel, M; Frade, R.
A; Note: 845-Arg and 1392-Thr were also found
R; Hermann, D; Barel, M; Frade, R.
A; Note: 845-Arg and 1392-Thr were also found
R; Hermann, D; Barel, M; Frade, R.
A; Residuc; 1910-929 chere
A; Molecule type: protein
A; Molecule type: protein
A; Reference number: A33443; MUID:90285190
A; Title: Mapping the binding sites of human erythrocyte ankyrin for the anion exchanger
A; Molecule type: protein
A; Molecule type: Molecule type: protein
A; Molecule type: Molecule type: protein
A; Molecule type: Molecule t
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A; Cross-references: GDB:118737; OMIM:182900
A; Cross-references: GDB:118737; OMIM:182900
A; Cross-references: GDB:118737; OMIM:182900
A; Cross-references: GDB:118737; OMIM:182900
A; Superfamily: ankyrin: ankyrin: ankyrin: ankyrin: ankyrin: ankyrin: 2, erythrocyte form: 1 #status predicted <MAT1>
C; Keywords: alternative splicing; phosphoprotein
C; Keywords: alternative splicing; prospin: 2, erythrocyte #status predicted <MAT1>
F; 2-1512,1675-1881/Product: ankyrin: 2, erythrocyte #status predicted <MAT2>
F; 2-827/Region: anion exchange protein binding
F; 4-76/Domain: ankyrin repeat homology <AN02>
F; 77-109/Domain: ankyrin repeat homology <AN03>
F; 110-142/Domain: ankyrin repeat homology <AN04>
F; 110-109/Domain: ankyrin repeat homology <AN05>
F; 172-204/Domain: ankyrin repeat homology <AN05>
F; 172-204/Domain: ankyrin repeat homology <AN05>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N;Contains: ankyrin 2.2
C;Species: Homo sapiens (man)
C;Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 22-Jun-1999
C;Accession: S08275; A33219; PC2220; A35443
R;Lux, S.E.; John, K.M.; Bennett, V.
                                                                        EPEEITGPVDEETFLKAAVEGKMKVIEKFLADGGSADTCDQFRR-TALHRASLEGHMEIL 166
                                                                                                                                                                                                            167 EKLLDNGATVDFQDRLDCTAMHWACRGGHLEVVKLLQSHGADTNVRDKLLSTPLHVAVRT 226
                                                                                                                                                                                                                                                       330 EIDDIT--LDHLTPLHVAAHCGHHRVAKVLLDKGAKPNSRALNGFTPLHIACKKNHVRVM 387
          Gaps
                                                                                                                                                                                                                                                                                                                                                                                          227 GQVEIVEHFLSLGLEINARDREGDTALHDAVRLNRYKIIKLLLLHGADMMTKNLAGKTP
          3;
          87; Indels
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N;Alternate names: ankyrin 2.1, erythrocyte; ankyrin-R
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              Mismatches
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C;Species: Mus musculus (house mouse)
C;Date: 27-May-1994 #sequence_revision 03-Aug-1995 #text_change 13-Aug-1999
C;Accession: 83777; White, R.A.; Peters, L.L.; Hall, E.J.; Lux, S.E.; Barker, J.E.
J. Biol. Chem. 268, 9533-9540, 1993
A;Itile: Complex patterns of sequence variation and multiple 5' and 3' ends are found a A;Reference number: S37771; MUID:93252825
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        244 ARDREGDTALHDAVRLNRYKIIKLLLHGADMMTKNLAGKTPTDLVQ----LWQADT--- 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              756 AKTKNGYTPLHQAAQQGHTHIINVLLQHGAKPNATTANGNTALAIAKRLGYISVVDTLKV 815
                                                                          A;Residues: 1-3924 <RES>
A;Cross-references: EMBL:Z26634; NID:g406287; PIDN:CAA81387.1; PID:g406288
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      124 AAVEGKMKVIEKFLADGGSADTCDQFRRTALHRASLEGHMEILEKLLDNGATVDFQDRLD 183
                                                                                                                                                                                                          C; Keywords: alternative splicing
F;2-3924/Product: ankyrin 2, long form #status predicted <MAT>
F;2-1443,3585-3924/Product: ankyrin 2, short form #status predicted <MA2>
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                                      Status: preliminary; nucleic acid sequence not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13.9%; Score 234.5; DB 2; 29.5%; Pred. No. 1.3e-07; ative 32; Mismatches 100;
                                                                                                                                                                                                                                                                                                                                                <AN05>
                                                                                                                                                                                                                                                                                                                                                                                                     <AN08>
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                                                                                                                                                                                                                                                                                                                                                                                                                               <AN09>
                                                                                                                                                    A;Cross-references: GDB:127607; OMIM:106410
A;Map position: 4q25-4q27
C;Superfamily: ankyrin; ankyrin repeat homology
C;Keywords: alternative splicing
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A; Reference number: A49462; MUID: 94075409
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F;298-330/Domain: ankyrin repeat
F;331-363/Domain: ankyrin repeat
                                                                                                                                                                                                                                                                                                                                                F;191-223/Domain: ankyrin repeat F;232-264/Domain: ankyrin repeat
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F;397-429/Domain: ankyrin repeat
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                                                      mRNA
                    A49462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 562-594/Domain:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   F;595,627/Domain:
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C; Species: Mus musculus (house mouse)
C; Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 13-Aug-1999
C; Accession: 149502
E; Accession: 149502
E; White, R.A.; Birkenmeier, C.S.; Peters, L.L.; Barker, J.E.; Lux, S.E.
Mamm. Genome 3, 281-285, 1992
A; Title: Murine erythrocyte ankyrin cDNA: Highly conserved regions of the regulatory
A; Reference number: 149502; MUD:92345717
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A.(Cross.references: EMBL:X69063; NID:9311816; PIDN:CAA48801.1; PID:9311817
C; Superfamily: ankyrin; ankyrin repeat homology
C; Keywords: alternative splicing
F:48-80/Domain: ankyrin repeat homology <AN01>
F; 81-113/Domain: ankyrin repeat homology <AN02>
F:114-146/Domain: ankyrin repeat homology <AN05>
F:147-175/Domain: ankyrin repeat homology <AN05>
F:147-175/Domain: ankyrin repeat homology <AN05>
F:209-241/Domain: ankyrin repeat homology <AN10>
F:209-241/Domain: ankyrin repeat homology <AN10>
F:209-241/Domain: ankyrin repeat homology <AN10>
F:209-241/Domain: ankyrin repeat homology <AN11>
F:209-241/Domain: ankyrin repeat homology <AN11>
F:209-241/Domain: ankyrin repeat homology <AN14>
F:209-241/Domain: ankyrin repeat homology <AN15>
F:200-538/Domain: ankyrin repeat homology <AN15>
F:200-538/Domain: ankyrin repeat homology <AN15>
F:200-531/Domain: ankyrin repeat homology <AN15>
F:200-6531/Domain: ankyrin repeat homology <AN16>
F:200-6531/Domain: ankyrin repeat homology <AN18>
F:200-650-631/Domain: ankyrin repeat homology <AN18>
F:200-650-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 167 EKLLDNGATVDFQDRLDCTAMHWACRGGHLEVVKLLQSHGADTNVRDKLLSTPLHVAVRT 226
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A.Status: preliminary; translated from GB/EMBL/DDBJ
A.Status: preliminary; translated from GB/EMBL/DDBJ
A.Status: preliminary; translated from GB/EMBL/DDBJ
A.Status: 1-1862 <RES>
A.Cross-references: GB:M84756; NID:g191939; PIDN:AAA37236.1; PID:g191940
G:Genetics:
A.Gene: Ank-1
C.Superfamily: ankyrin ankyrin repeat homology
C.Keywords: alternative splicing
C.Keywords: alternative splicing
F.73-105/Domain: ankyrin repeat homology <AN02>
F.106-138/Domain: ankyrin repeat homology <AN03>
F.106-138/Domain: ankyrin repeat homology <AN04>
F.139-167/Domain: ankyrin repeat homology <AN04>
F.139-167/Domain: ankyrin repeat homology <AN04>
F.139-167/Domain: ankyrin repeat homology <AN04>
F.106-136/Domain: ankyrin repeat homology <AN04>
F.106-136/F.106-136/F.106-136/F.106-136/F.106-136/F.106-136/F.106-136/F.106-136/F.106-136/F.106-136/F.106-136/F.106-136/F.106-136/F.106-136/F.106-136/F.106-136/F.106-136/F.106-136/F.106-136/F.106-136/F.106-136/F.106-136/F.106-136/F.106-136/F.106-136/F.106-136/F.106-136/F.106-136/F.106-136/F.106-136/F.106-136/F.106-136/F.106-136/F.106-136/F.106-136/F.106-136/F.106-136/F.106-136/F.106-136/F.106-136/F.106-136/F.106-136/F.106-136/F.106-136/F.106-136/F.106-136/F.106-136/F.106-136/F.106-136/F.106-136/F.106-136/F.106-136/F.106-136/F.106-136/F.106-136/F.106-136/F.106-136/F.106-136/F.106-136/F.106-136/F.106-136/F.106-136/F.106-136/F.106-136/F.106-136/F.106-136/F.106-136/F.106-136/F.106-136/F.106-136/F.106-136/F.106-136/F.106-136/F.106-136/F.106-136/F.106-136/F.106-136/F.106-136/F.106-136/F.106-136/F.106-136/F.106-136/F.106-136/F.106-136/F.106-136/F.106-136/F.106-136/F.106-136/F.106-136/F.106-136/F.106-136/F.106-136/F.106-136/F.106-136/F.106-136/F.106-136/F.106-136/F.106-136/F.106-136/F.106-136/F.106-136/F.106-136/F.106-136/F.106-136/F.106-13
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C:Species: Mus musculus (house mouse)
C:Species: Mus musculus (house mouse)
C:Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 04-Mar-2000
C:Accession: T42715
R:Peters, L.L., John, K.M.; Lu, F.M.; Eicher, E.M.; Higgins, A.; Yialamas, M.; Turtzo J. Cell Biol. 130, 313-330, 1995
A;Title: Ank3 (epithelial ankyrin), a widely distributed new member of the ankyrin ge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Reference number: Z22237; MUID:95340633
A; Accession: T42715
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: mRNA
A; Residues: 1-1940 (>PET>
A; Rosidues: 1-1940 (>PET>
A; Cross-references: EMBL:L40632; NID:g710548; PID:g710549; PIDN:AAB01604.1
A; Experimental source: strain C57BL/6J; kidney
C; Genetics: Ank3
A; Map position: 10
A; Introns: 83471
C; Superfamily: ankyrin; ankyrin repeat homology
C; Superfamily: ankyrin; splicing
C; Keywords: alternative splicing
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        316 NGLSPLHMATQGDHLNCVQLLLQHNVPVDDVTNDYLTALHVAAHCGHYKVAKVLLDKKAS 375
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376 PNAKALNGFTPLH----IACKKNRIRVMELLLKHGASIQAVTESGLTPIHVAAFMGHVN 430
                                                                22 EENEKLRGDTRQKL-PMDLLVLEDEKHHGAQSAALQKVKGQERVRKTSLDLRREIID--- 77
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                                                                                                                                               165 ILEKLIDNGATVDFQDRLDCTAMHWACRGGHLEVVKLLQSHGADTNVRDKLLSTPLHVAV
                                                                                                                     225 RTGQVEIVEHFLSLGLEINARDREGDTALHDAVRLNRYKIIKLLLLHGADMMTKNLAGKT
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llarity 25.9%; Pred. No. 1.1e-07;
Conservative 41; Mismatches 124;
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ankyrin 3, splice form 1 - mouse
C;Species: Mus musculus (house mouse)
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nes 78; Conserv
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C; Species: Mus musculus (house mouse)
C; Species: Il-dan-2000 #sequence_revision 11-Jan-2000 #text_change 04-Mar-2000
C; Accession: T42714
R; Peters, L.L.; John, K.M.; Lu, F.M.; Eicher, E.M.; Higgins, A.; Yialamas, M.; Turtzo, I.J. Cell Biol. 130, 313-330, 1995
A; Title: Ank3 (epithelial ankyrin), a widely distributed new member of the ankyrin gene
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A;Experimental source: strain C57BL/6J; kidney
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     167 EKLLDNGATVDFQDRLDCTAMHWACRGGHLEVVKLLQSHGADTNVRDKLLSTPLHVAVRT 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EPEEITGPVDEETFLKAAVEGKMKVIEKFLADGGSADTCDQFRR-TALHRASLEGHMEIL 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               326 EIDDIT--LDHLTPLHVAAHCGHRVAKVLLDKGAKPNSRALNGFTPLHIACKKNHIRVM 383
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; Pred. No. 9.8e-08;
41; Mismatches 124;
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A; Accession: T42714
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F;597-629/Domain: ankyrin repeat hc
F;630-662/Domain: ankyrin repeat hc
F;663-695/Domain: ankyrin repeat hc
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A; Residues: 1-1765 <PET>
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Introns: 1587/1
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                                                                                                F;432-464/Domain:
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                                                                                                                                                          F;531-563/Domain:
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C; Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 04-Mar-2000 C; Accession: T42713 R; Peters, L.L.; John, K.M.; Lu, F.M.; Eicher, E.M.; Higgins, A.; Yialamas, M.; Turtzo, I J. Cell Biol. 130, 313-330, 1995 A; Title: Ank3 (epithelial ankyrin), a widely distributed new member of the ankyrin gene; the repeat domain.
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A;Title: Ank3 (epithelial ankyrin), a widely distributed new member of the ankyrin gene
                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Description: supposed to play an important role in the polarized distribution of many A; Note: major Kidney ankyrin C; Superfamily: ankyrin; ankyrin repeat homology C; Keywords: alternative splicing
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Spate: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 04-Mar-2000
Accession: T42716
                                                                                                                                                   A; Reference number: 22237; MUID:95340633
A; Reference number: 22237; MUID:95340633
A; Accession: T42713
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: mRNA
A; Residues: 1-1943 <PET>
A; Cross-references: EMBL:L40632; NID:9710548; PID:9710550; PIDN:AAB01606.1
A; Experimental source: strain C57BL/6J; kidney
C; Genetics:
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A;Experimental source: strain C57BL/6J; kidney
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ILEKLLDNGATVDFQDRLDCTAMHWACRGGHLEVVKLLQSHGADTNVRDKLLSTPLHVAV 224
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A;Molecule type: mRNA
A;Residues: 1-1961 <PET>
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A;Gene: Ank3
A;Map position: 10
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C;Superfamily: ankyrin; ankyrin repeat homology
C;Keywords: alternative splicing
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173.5 173.5 173.5 173.1 173.1 173.1 171.5 171.5 169.5 169.5 169.5 167.5 169.5		HUMAN V379_HUMAN V379_HUMAN C015084 Z0-AUG-2001 (Re- Z0-A
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modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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D32115487A80839F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               117 DEETFLKAAVEGKMKVIEKFLADGGSADTCDQFRRTALHRASLEGHMEILEKLLDNGATV 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           177 DFQDRLDCTAMHWACRGGHLEVVKLLQSHGADTNVRDKLLSTPLHVAVRTGQVEIVEHFL 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lux S.E., John K.M., Bennett V., "Analysis of cDNA for human erythrocyte ankyrin indicates a repeated structure with homology to tissue-differentiation and cell-cycle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-APR-1990 (Rel. 14, Created)
01-APR-1990 (Rel. 14, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
ANKYRIN 1 (ERYTHROCYTE ANKYRIN) (ANKYRIN R) (ANKYRINS 2.1 AND 2.2).
ANKIR OR ANK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
MEDLINE-901737370; PubMed=1689849;
MEDLINE-901737370; PubMed=1689849;
Cheung M.C., Kan Y.W., Palek J.;
Cheung M.C., Kan Y.W., Palek J.;
                                                                                                                                                                                                                                         79; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        237 SLGLEINARDREGDTALHDAVRLNRYKIIKLLLLHGADMMTKNLAGKTPTD 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 692;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A., PARTIAL SEQUENCE, AND VARIANTS.
TISSUE-Hematopoietic;
MEDLINE-90158830; PubMed=2137557;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14.5%; Score 245; DB 1; 32.7%; Pred. No. 1.1e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT; 1880 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               36; Mismatches
                                                                               EMBL; AB023174; BAA76801.1; EMBL; AL117504; CAB55968.1; EMBL; AL1096678; CAB8658.1; HSSP; Q00421; 1AWC. InterPro; IPR002110; ANK. PEIN; PR01415; ANK. PRINTS; PR01415; ANK. KINSRINT; SM00248; ANK; 6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              87
75722
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Matches 56; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nature 344:36-42(1990).
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103
1169
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 692 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ANK1_HUMAN
P16157;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CONFLICT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VARSPLIC
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                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 184 CTAMHWACRGGHLEVVKLLQSHGADTNVRDKLLSTPLHVAVRTGQVEIVEHFLSLGLEIN 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        124 AAVEGKMKVIEKFLADGGSADTCDQFRRTALHRASLEGHWEILEKLLDNGATVDFQDRLD 183
                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   240 EPNAYGNTPLHVACYNGODVVVNELIDCGAIVNOKNEKGFTP---LHFAAASTHGAL 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (Human).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.
-!- ALTERNATIVE PRODUCTS: 2 ISOFORMS; 1 (SHOWN HERE) AND 2; MAY
PRODUCED BY ALTERNATIVE SPLICING.
                                                                                                                                                                                                                                                                                                                                                                                  3;
                                                                                                                                                                                                                                                                                                                                            Length 1059;
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                     K 15.

K 16.

K 17.

K 19.

K 19.

K 20.

K 21.

K 22.

K 23.

K 24.

K 25.

K 26.

K 26.

K 27.
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Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                            16.8%; Score 284.5; DB 1;
37.3%; Pred. No. 3.5e-12;
:ive 32; Mismatches 76;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 2
Y957_HUMAN STANDARD; PRT; 692 AA.
ID V957_HUMAN STANDARD; PRT; 692 AA.
O9Y264; 09NU24; 09UF09;
DT 20-AUG-2001 (Rel. 40, Created)
DT 20-AUG-2001 (Rel. 40, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last sequence update)
DF 20-AUG-2001 (Rel. 40, Last annotation update)
DF 19POTHETICAL PROTEIN KIAA0957.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 140-692 FROM N.A. (ISOFORM 1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 87-692 FROM N.A. (ISOFORM 2).
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857
                           510 54 555 588 5110 554 555 588 518 611 754 755 751 751 751 828 851 861 895 931 905 943;
                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
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REPEAT
SEQUENCE
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MISSING (IN ISOFORM 2.2).
H -> D (IN ISOFORM 2.2).
H -> D (IN ISOFORM 2.2).
GLOGDLEDPSELEVDIDYFWKHSKDHTSTPNP -> ELRGS
GLOPDLIEGRKGAQIVKRASLKRGKO (IN A THIRD
ISOFORM).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       167 EKLLDNGATVDFQDRLDCTAMHWACRGGHLEVVKLLQSHGADTNVRDKLLSTPLHVAVRT 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          108 EPEEITGPVDEETFLKAAVEGKMKVIEKFLADGGSADTCDQFRR-TALHRASLEGHMEIL 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  227 GQVEIVEHFLSLGLEINARDREGDTALHDAVRLNRYKIIKLLLLHGADMMTKNLAGKTP 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ANK2_HUMAN STANDARD; PRT; 3924 AA.
001484; Q01485;
01-APR-1993 (Rel. 25, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
ANKYRIN 2 (BRAIN ANKYRIN) (ANKYRIN B) (ANKYRIN, NONERYTHROID).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 M -> S (IN REF. 2).
V -> I (IN REF. 2).
W, 1C5F5E7EFDICD428 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          D -> N (IN DUESSELDORF).
/FTId=VAR_000602.
                                                                                                                                                                                                                                                                                                                                                              v -> I (IN HS).
/FTId=VAR_000596.
R -> H (IN BRUEGGEN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13.9%; Score 234.5; DB 1; 33.5%; Pred. No. 2e-08;
                                                                                                                                                                                                                                                                                                                                                  FTIG-VAR_000595.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /FTId=VAR_000601
                                                                                                                                                                                                                                                                                                                                                                                                           /FTId=VAR_000597
                                                                                                                                                                                                                                                                                                                                                                                                                                        FTIG-VAR_000598
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FTIG=VAR_000600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /FTId-VAR_000603
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E
            ANK 8.

ANK 9.

ANK 11.

ANK 11.

ANK 12.

ANK 13.

ANK 14.

ANK 16.

ANK 16.

ANK 17.

ANK 18.

ANK 18.

ANK 18.

ANK 20.

ANK 21.

ANK 21.

ANK 21.

ANK 21.

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ANK 21.
                                                                                                                                                                                                                                                DEATH.
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Best Local Similarity 33.55
Matches 60; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1285
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Homo sapiens (Human).
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1880 AA;
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SEQUENCE
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                                             MEDLINE-9022460; PubMed-8640229;
REDELINE-9022460; PubMed-8640229;
REDELINE-9022460; PubMed-8640229;
REDELINE-9022460; M.V. Lux M.L., Scarpa A.L., Tse W.T.,
A Gallagher P.G., Schroeter W., Forget B.G., Lux S.E.;
Tankyrin-1 mutations are a major cause of dominant and recessive hereditary spherocytosis.";
I MARYTIN-1 mutations are a major cause of dominant and recessive control of the process of the properties of the control of the control
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                                                                                                                                                                                                                                                                                                                                      -!- PTM: REGULATED BY PHOSPHORYLATION.
-!- PTM: ACYLATED BY PALMITIC ACID GROUP(S).
-!- DISEASE: DEFECTS IN ANKI ARE THE CAUSE OF DOMINANT AND RECESSIVE HEREDITARY SPHEROCYTOSIS (4S).
-!- SIMILARITY: CONTAINS 13 ANK REPEATS.
-!- SIMILARITY: CONTAINS 1 DEATH DOMAIN.
                                                                                                                                                                                                                                                                                            ALTERNATIVE PRODUCTS: VARIOUS ISOFORMS OF ANKYRIN ARE PRODUCED ALTERNATIVE SPLICING. THE SEQUENCE SHOWN IS THAT OF ANKYRIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     89 KDA DOMAIN (ANION EXCHANGE PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cytoskeleton; Alternative splicing; Repeat; ANK repeat;
Phosphorylation; Lipoprotein; Multigene family; Discase mutation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            55 KDA REGULATORY DOMAIN (REGULATES THE BINDING OF ANKYRIN TO SPECTRIN AND THE BAND 3 PROTEIN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   62 KDA DOMAIN (SPECTRIN BINDING
    "cDNA sequence for human erythrocyte ankyrin.";
Proc. Natl. Acad. Sci. U.S.A. 87:1730-1734(1990)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BINDING DOMAIN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE; PS50088; ANK_REPEAT; 20. PROSITE; PS50297; ANK_REP_REGION; 1. PROSITE; PS50017; DEATH_DOMAIN; 1.
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Elliptocytosis; Polymorphism.
INII_MET 0 0
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InterPro; IPR000488; Death.
InterPro; IPR000906; ZU5.
Pfam; PF00023; ank; 23.
Pfam; PF00731; death; 1.
Pfam; PF00791; ZU5; 1.
SMART; SM00248; ANK; 22.
SMART; SM0005; ZU5; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; X16609; CAA34610.1; -. EMBL; M28880; AAA51732.1; -.
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PIR; A35049; A35049.
HSSP; Q00420; IAWC.
MIM; 182900;
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SMART; SM00005; DEATH; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                       CELLS THROUGHOUT THE BRAIN.

THE DRAIN.

THE BRAIN.

AND EACH PROSPRORYLATED AT MULTIPLE SITES BY DIFFERENT PROTEIN KINASES AND EACH PROSPHORYLATION EVENT REGULATES THE PROTEIN'S STRUCTURE AND FUNCTION (POTENTIAL)
                                                                                                                                                                                                                                                                                    TISSUE=Brain stem;
MEDLINE=94075409; PubMed=8253844;
Chan W., Kordell E., Bennett V.;
Chan WankyrinB: structure of the major developmentally regulated domain and selective localization in unmyelinated axons.";
J. Cell Biol. 123:1463-1473(1993).
     Chordata; Craniata; Vertebrata; Euteleostomi;
Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                            MEDLINE-92009921; PubMed-1833308;
Tse W.T., Menninger J.C., Yang-Feng T.L., Francke U., Sahr K.E.,
Lux S.E., Ward D.C., Forget B.G.;
                                                                                                                                                                                                                                                                          "Isolation and chromosomal localization of a novel nonerythroid
                                                                                                                                                           human brain
                                                                                                                                                                     genes.
                                                                                                                                                                                                            Carpenter S.; Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases
                                                                                                                                  TISSUE=Brain stem;
MEDLINE-91302466; PubMed=1830053;
Otto E., Kunimoto M., McLaughlin T., Bennett V.;
"Isolation and characterization of cDRAs encoding ankrins reveal a family of alternatively spliced J. Cell Biol. 114:241-253(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                AND FUNCTION (POTENTIAL).
SIMILARITY: CONTAINS 23 ANK REPEATS.
SIMILARITY: CONTAINS 1 DEATH DOMAIN.
                                                                                                                       SEQUENCE FROM N.A. (ISOFORMS 1; 2 AND 3).
                                            SEQUENCE FROM N.A. (ISOFORM 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; Z26634; CAB42644.1; -.
                                                                                                                                                                                                                                        SEQUENCE OF 463-495 FROM N.A.
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X56958; CAA40279.2;
M37123; AAA62828.1;
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; PF00531; death; 1.
; PF00791; ZUS; 1.
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InterPro; IPR000488;
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PIR; A39643; A39643.
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PIR; S14569; S14569.
HSSP; Q00420; 1AWC.
        Eukaryota; Metazoa;
Mammalia; Eutheria;
                           NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              M37123;
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244 ARDREGDTALHDAVRLINRYKIIKLLLLHGADMMTKNLAGKTPTDLVQ----LWQADT--- 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 124 AAVEGKMKVIEKFLADGGSADICDQFRRTALHRASLEGHMEILEKLLDNGAIVDFQDRLD 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0 -> QFLGKLHLPTAPPPLNEGESLVSRILQLGPPGTK
(IN ISOFORM 2).
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QY -> HA (IN REF. 2).
II -> Y (IN REF. 2).
MW; 52AC496C428E39D2 CRC64;
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                                 Cytoskeleton; Alternative splicing; Repeat; ANK repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (APPROXIMATE)
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PROSITE; PS50088; ANK REPEAT; 20. PROSITE; PS50297; ANK REP_REGION; 1. PROSITE; PS50017; DEATH_DOMAIN; 1.
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                                                Phosphorylation; Multigene family
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Matches 65; Conservative
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                                                                                                                                                                                                                                                                                         regulatory domain."

Meann. Genome 3:281-285(1992).

-!- FUNCTION: ATTACH INTEGRAL MEMBRANE PROTEINS TO CYTOSKELETAL

-!- FUNCTION: ATTACH INTEGRAL MEMBRANE PROTEIN BAND 4.2, TO

BLEMENTS; BIND TO THE ENYTHROCYTE MEMBRANE PROTEIN BAND 4.2, TO

NA-K ATPASE; TO THE LYMPHOCYTE MEMBRANE PROTEIN GP85, AND TO THE

CYTOSKELETAL PROTEINS FODELN, VIBENTIN AND DESMIN.

ERYTHROCYTE ANKYRINS ALSO LINK SPECTRIN (BETA CHAIN) TO THE

CYTOPLASMIC DOMARIN OF THE ENYTHROCYTES ANION EXCHANGE PROTEIN;

THEY RETAIN MOST OR ALL OF THESE BINDING FUNCTIONS.

-!- SUBCELLULAR LOCATION: CYTOPLASMIC SURPACE OF ERYTHROCYTIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE; PS50088; ANK_REPEAT; 20.
PROSITE; PS50297; ANK_REP_REGION; 1.
PROSITE; PS50017; DEATH_DOMAIN; 1.
Cytoskeleton; Repeat; ANK repeat; Phosphorylation; Lipoprotein.
DOMAIN 1 827 B9 KDA DOMAIN (ANION EXCHANGE PROTEIN BINDING DOMAIN).
                                                                                                                                                                    Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                            TISSUE-Erythrocyte;
BEDLINE-92345717; PubMed-1386265;
White R.A., Birkenmeler C.S., Peters L.L., Barker J.E., Lux S.E.;
"Murine erythrocyte ankyrin cDNA: highly conserved regions of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              55 KDA REGULATORY DOMAIN (REGULATES THE BINDING OF ANKYRIN TO SPECTRIN AND THE BAND 3 PROTEIN).
ANK 1.
ANK 2.
                                                                                                                                                                                                                                                                                                                                                                                                                          -:- PTM: REGULATED BY PHOSPHORYLATION (BY SIMILARITY).
-:- PTM: ACYLATED BY PALMITTC ACID GRODP(S) (BY SIMILARITY).
-:- SIMILARITY: CONTAINS 23 ANK REPEATS.
-:- SIMILARITY: CONTAINS 1 DEATH DOMAIN.
-----RHALEHPEPGAEHNGLEGPNDSGRET 322
              815 VTEEVTTTTTTTTTTEKKKINVPETMTE--VLDVSDEEGDDT 853
                                                                                                                      Last sequence update)
Last annotation update)
                                                                                    PRT; 1862 AA
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ANKI OR ANK-1.
                                                                                                           Created)
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Pfam; PF00031; death; 1.
Pfam; PF00791; 205; 1.
SMART; SM00048; ANK; 22.
SMART; SM00005; DEATH; 1.
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InterPro; IPR000488; Death.
InterPro; IPR000906; 2U5.
                                                                                    STANDARD;
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                                                                                                                      (Rel. 32,
                                                                                                                                                                                                                                                                                                                                                                                                               PLASMA MEMBRANE.
                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                        NCBI_TaxID=10090;
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                                                                                                         01-NOV-1995
01-NOV-1995
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                                                                                  ANK1_MOUSE
Q02357;
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20-AUG-2001 (Rel. 40, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
NF-KAPPAB INHIBITOR ALPHA (L'KAPPA-B-ALPHA) (IKAPPABALPHA) (IKB-ALPHA)
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MEDLINE=91368196; PubMed=1891714;
Davis N., Ghosh S., Simmons D.L., Tempst P., Liou H.-C., Baltimore D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SCIENCE 253:1268-1271(1991).

SCIENCE 253:1268-1271(1991).

-1- FUNCTION: INHIBITOR OF NF-KAPPA-B THAT TIGHTLY REGULATES NF-KAPPA-B ACTIVATION BY COMPLEXING AND TRAPPING IT IN THE CYTOPLASM. MAY BE INVOLVED IN REGULATION OF TRANSCRIPTIONAL RESPONSES TO NF-KAPPA-B, INCLUDING CELL ADHESION, IMMUNE AND PROINFLAMMATORY RESPONSES, APOPTOSIS, DIFFERENTIATION AND GROWTH. CONTROLLED BY SEQUENTIAL SERINE-PHOSPHORYLATION, UBIODITINATION AND DEGRADATION. TYROSING-PHOSPHORYLATION COULD ONLY LEAD TO DISSOCIATION FROM NF-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          108 EPEEITGPVDEETFLKAAVEGKMKVIEKFLADGGSADTCDQFRR-TALHRASLEGHMEIL 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EKLLDNGATVDFQDRLDCTAMHWACRGGHLEVVKLLQSHGADTNVRDKLLSTPLHVAVRT 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     227 GQVEIVEHFLSLGLEINARDREGDTALHDAVRLNRYKIIKLLLLHGADMMTKNLAGKTP 285
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Matches 61; C
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181
20-AUG-2001 (Rel. 40,
20-AUG-2001 (Rel. 40,
20-AUG-2001 (Rel. 40,
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768 AA;
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Best Local Similarity
Matches 77; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12;
                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                        use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            211 VRDKLLSTP-----LHVAVRTGQVEIVEHFLSLGLEINARDR-EGDTALHDAVRLNRYK 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100 AASHEPPPEP----EEITGPVDEETFLKAAV--EGK---MKVIEKFLADGGSADTCDQFR 150
                                                                                                                                                                                                                                                                                                                                                                                                             PHOSPHORYLATION (BY IKKA, IKKB AND IKKE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              40 LVLEDEKHHGAQSAALQKVKGQERVRKTSLDLRREIIDVGGIQNLIELRKKRKQKKRDAL 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61
                                                                  PTM: SUBSEQUENT TO STIMULUS-DEPENDENT PHOSPHORYLATION ON SERINES, POLYUBIQUITINATION TARGETS THE PROTEIN FOR RAPID DEGRADATION VIA THE UBIOQUITIN SYSTEM (BY SIMILARITY).
SIMILARITY: BELONGS TO THE NE-KAPPA-B INHIBITOR FAMILY.
SIMILARITY: CONTAINS 4 ANK REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           62 ----EPPARPHAWAQQLT--EDGDTFLHLAIIHEEKALSLEVIRQAAGDAAFLNFQNNLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RTALHRASLEGHMEILEKLLDNGATVDFQDRLDCTAMHWACRGGHLEVVKLLQSHGADTN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUBCELLUTAR LOCATION: CYTOPLASMIC.
TISSUE SPECIFICITY: HIGHLY EXPRESSED IN LYMPH NODE, THYMUS
FOLLOWED BY LIVER, BRAIN, MUSCLE, KIDNEY, GASTROINTESTINAL AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  27 LLPPDDRH----BSGLDSMK-BEEYRQ----LVRELEDI-------RLQPR----
                                                                                                                                                                                                                                                                                                                                                                                       PHOSPHORYLATION (BY IKKA AND IKKB)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           49:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13.5%; Score 228.5; DB 1; Length 318; 29.8%; Pred. No. 5.5e-09; tive 43; Mismatches 99; Indels 49
                                                                                                                                                                                                                                                                                                                                                                                                                             (BY SIMILAKITY).
PHOSPHORYLATION (BY TYR-KINASES)
                                                                                                                                                                                                                                                                                                                                                                               UBIQUITIN (BY SIMILARITY).
                SUBUNIT: INTERACTS WITH P65 (RELA) (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                             3Y SIMILARITY).
ZEF1BFB21B54E29F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  768 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                         SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      264 IIKLLLLHGADMMTKNLAGKTPTDLVQLWQAD 295
                                                                                                                                                                                                                                                                                                                                                                                                     SIMILARITY)
                                                                                                                                                                                                                                                                                     PRINTS, FRALELL,

SMOD248; ANK, 4.

PROSITE; PS50088; ANK_REP_REGION, 1.

PROSITE; PS50297; ANK_REP_REGION, 1.

Phosphorylation; ANK repeat, ANK 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                              (BY
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                                                                                                                                                                                                                          EMBL; S55765; AAB19758.1; -. EMBL; M74544; AAA49030.1; -.
        KAPPA-B (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                        35398
                                                                                                                                                                                                                                                          Interpro; IPR002110; ANK. Pfam; PF00023; ank; 5. PRINTS; PR01415; ANKYRIN.
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                                                              REPRODUCTIVE TRACT.
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215
249
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36
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                                                                                                                                                                                                                                                  HSSP; P25963; 11KN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         318 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                     46
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Q9ULJ7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
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REPEAT
BINDING
MOD_RES
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CTAMHWACRGGHLEVVKLLQSHGADTNVRDKLLSTPLHVAVRTGQVEIVEHFLSLGLEIN 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        204 ALIEQGARTNEI-----DNDGRIP--FILASQEGHYDCVQILLENKSNIDQRGYDGRNA 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        64 VRKTSLDLRREIIDVGGIQNLIELRKKRKQKKRDALAASHEPPPEFEITGPVDEETFLK 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         53; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                              "prediction of the coding sequences of unidentified human genes. XV The complete sequences of 100 new cDNA clones from brain which code for large proteins in vitro.";

DNA Res. 6:337-345(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12 ALIEQRLAQEEENEKLRGDTRQKLPMDLLVLEDEKHHGAQSAALQK-----VKGQER
                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCE._TaxID-9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 768;
                                                                                                                                                                                                                                                                                                                                                      MEDLINE-20039619; Pubmed-10574462;
Nagase T., Ishikawa K.-I., Kikuno R., Hirosawa M., Nomura N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Res. 6:337-345(1999).
SIMILARITY: CONTAINS AT LEAST 14 ANK REPEATS.
20-AUG-2001 (Rel. 40, Last sequence update) 20-AUG-2001 (Rel. 40, Last annotation update) HYPOTHETICAL PROTEIN KIAA1223 (FRAGMENT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR002110; ANK.
Pfam: PF00023; ank; 13.
PART; SM00248; ANK; 13.
PROSITE; PS50088; ANK_REPERT; 13.
PROSITE: PS50297; ANK_REP_REGION; 1.
Hypothetical protein; Repeat; ANK repeat.
NOW_TER 1 1 1 2 NNK 1
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RESULT 9
RN5A_HUMAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                  FUNCTION: MEDIATES THE EFFECTS OF INTERFERON AGAINST PLOCRANTHRUGES. ACTIVE WHEN BOUND TO 2-56 (5'-PHOSPHORYLATED 2',5'-LINKED OLIGOADENTAPES). CAPABLE OF CLEAVING POLY(RU) AND, TO A LESSER EXTENT, POLY(RA), TO SETS OF DISCRETE PRODUCTS RANGING PROM BETWHERN 4 AND 22 NUCLEOTIDES IN LENGTH.

CATALYTIC ACTIVITY: CLEAVES 3' OF UNP DIMERS, WITH PREFERENCE FOR UN AND UN AND UN SEQUENCES.
352 RSALQSAAWQGHVKVVQLLIEHGAVVDHTCNQGATALCIAAQEGHIDVVQVLLEHGADPN 411
                                 244 ARDREGDTALHDAVRLNRYKIIKLLLHGADMMTKNLAGKTPTDLVQLWQADTRHALE 301
                                                                                                                                                                                                                                             SEQUENCE FROM N.A. MEDLINE-93201598; PubMed-7680958; Zhou A., Hassel B.A., Silverman R.H.; Expression cloning of 2-5A-dependent RNAase: a uniquely regulated mediator of interferon action."; Cell 72:753-765(1993).
                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                 COFACTOR: OPTIMAL RNA CLEAVAGE RATES REQUIRES THE PRESENCE OF EITHER MANGANESE OR MAGNESIUM AND ATP.
                                                                                                                                 01-NOV-1995 (Rel. 32, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
2-5A-DEPENDENT RIBONUCLEASE (EC 3.1.26.-) (2-5A-DEPENDENT RNASE)
(RIBONUCLEASE L) (RNASE L) (RIBONUCLEASE 4) (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE; PS50088; ANK_REPEAT; 7.
PROSITE; PS50297; ANK_REP_REGION; 1.
PROSITE; PS50211; PROTEIN_KINASE_DOM; 1.
Hydrolase, Nuclease; RNA-binding; Endonuclease; Zinc-finger;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2-5A BINDING (P-LOOP) 1.
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                                                                                                   679 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                             SIMILARITY: CONTAINS 9 ANK REPEATS.
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Interpro; IPR002110; ANK.
Interpro; IPR000719; Euk_pkinase.
                                                                                                                        01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequ
20-AUG-2001 (Rel. 40, Last anno
                                                                                                                                                                                                                                                                                                                                                                                                                                  INDUCTION: BY INTERFERON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; L10382; AAA37117.1; -.
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Pfam; PF00069; pkinase; 1.
                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SMART; SM00248; ANK; 7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             53
87
1120
1153
1197
2268
3301
3328
584
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                                                                                                                                                                                             (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Repeat; ANK repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q00420; 1AWC.
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91
124
167
201
                                                                                                                                                                                 RNASEL OR RNS4
                                                                                                                                                                                             Mus musculus
                                                                                                   RN5A_MOUSE
Q05921;
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-i- FUNCTION: MEDIATES THE EFFECTS OF INTERFERON AGAINST
DICORRAVIRGES. ACTIVE WHEN BOUND TO 2-5A (5'-PHOSPHORYLATED
2',5'-LINKED OLIGOADENYLATES). CAPABLE OF CLEAVING POLY(RU) AND,
TO A LESSER EXTENT, POLY(RA), TO SETS OF DISCRETE PRODUCTS RANGING
FROM BETWEEN 4 AND 22 NUCLEOTIDES IN LENGTH.
--- CAPALYTIC ACTIVITY: CLEAVES 3' OF UPP DIMERS, WITH PREFERENCE
FOR UT AND UA SEQUENCES.
--- COFACTOR: OPTIMAL RNA CLEAVAGE RATES REQUIRES THE PRESENCE OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              70 GRVDIVNLLLSHGADPHRRKKNGAT---PFIIAGIQGDVKLLEILLSCGADVNECDENGF 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LL-DNGATVDFQDR-----LDCTAMHWACRGGHLEVVKLLQSHGADTNVRDKLLSTPLHV 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -----TALHRASLEGHMEILEK 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     127 TAFMEAAERGNAEALRFLFAKGANVNLRRQTTKDKRRLKQGGATALMSAAEKGHLEVLRI 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AVRTGQVEIVEHFLSL-GLEINARDREGDTALHDAVRLNRYKIIKLLLLHGADMMTKNLA 281
                                                                                                                                                                                                                                                                                                                                                                                                94 KKRDA--LAASHEPPPEPEEITGPVDEETFLKAAVEGKMKVIEKFLADGGSADTCDQ--- 148
                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                            22 VVEDD-----SSLIKAVQKGDVVRV-----QQLLEKGADANACEDTWGWTPLHNAVQA 69
                                                                                                                                                                                                                                                                                  41 VLEDEKHHGAQSAALQKVKGQERVRKTSLDLRREIIDVGGIQNLIE-----LRKKRKQ 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE=Kidney;
MEDLINE-93201588; PubMed=7680958;
Abou A., Hassel B.A., Silverman R.H.;
"Expression cloning of 2-5A-dependent RNMase: a uniquely regulated mediator of interferon action.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-FEB-1996 (Rel. 33, Last sequence update)
20-A016-2001 (Rel. 40, Last annotation update)
2-54-DEPENDENT RIBONUCLEASE (EC 3.1.26.-) (2-5A-DEPENDENT RNASE)
(RIBONUCLEASE L) (RNASE L) (RIBONUCLEASE 4).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Intrinsic molecular activities of the interferon-induced 2-5A-
                                                                                                                                                                                                                            96;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-94245737; PubMed-7514601;
Dong B., Xu L., Zhou A., Hassel B.A., Lee X., Torrence P.F.,
Silverman R.H.;
                                                                                                                                                                 Length 679;
                                                                                                                                                                    13.2%; Score 224; DB 1; Length 67
28.1%; Pred. No. 2.9e-08;
.ive 41; Mismatches 101; Indels
                                                                                      507DB36B62EC1F4D CRC64;
2-5A BINDING (P-LOOP) 2. C6-TYPE (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  741 AA
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J. Biol. Chem. 269:14153-14158(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-NOV-1995 (Rel. 32, Created)
                                                                                      76800 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   282 GKTPTDLVQLWQADTRH 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ----DDLV--WIARRNH 311
                                                                                                                                                                                                                                  89; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cell 72:753-765(1993).
                                                              619
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens (Human).
                                                           679 (
679 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CHARACTERIZATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RNASEL OR RNS4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RN5A_HUMAN
Q05823;
     DOMAIN
ZN_FING
NON_TER
SEQUENCE
                                                                                                                                                                             Query Match
                                                                                                                                                                                                       Best Local
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                                                                                                                                                                                                                                                      "Nucleotide sequence of the heme subunit of flavocytochrome c from the purple phototrophic bacterium, Chromatium vinosum. A 2.6-kilobase pair DNA fragment contains two multiheme cytochromes, a flavoprotein, and a homolog of human ankyrin.";
J. Blol. Chem. 268:14422-14431(1993).
-!- SIMILARITY: CONTAINS 8 ANK REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      133 DALMIASRHGITDMVEQLLFKGADPKAADREGRTALMQAASKGETGVLPLLIEGGADLEA 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          119 ETFLKAAVEGKMKVIEKFLADGGSADTCDQFRRTALHRASLEGHMEILEKLLDNGATVDF 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QDRLDCTAMHWACRGGHLEVVKLLQSHGADTNVRDKLLSTPLHVAVRTGQVEIVEHFLSL 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         239 GLEINARDREGDTALHDAVRLNRYKIIKLLLHGADMMTKNLAGKTPTDL-VQLWQADTR 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4
                                                                                                                 Bacteria; Proteobacteria; gamma subdivision; Chromatiaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 323;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  88; Indels
                                                                                                                                                                                                                          Dolata M.M., van Beeumen J.J., Ambler R.P., Meyer T.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3976D34A9BD607DF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12.7%; Score 215; DB 1; 32.6%; Pred. No. 4.7e-08;
                                   (Rel. 31, Created)
(Rel. 31, Last sequence update)
(Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               POTENTIAL.
ANKYRIN HOMOLOG.
            323 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             36; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ANK
ANK
ANK
ANK
                                                                                                                                                                                           STRAIN=D / ATCC 17899 / DSM 180;
MEDLINE=93300842; PubMed=8390993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    33453 MW;
                                                                                    ANKYRIN HOMOLOG PRECURSOR.
           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    229
262
323 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                  Chromatium vinosum
                                   01-FEB-1995 (Rel. 01-FEB-1995 (Rel. 20-AUG-2001 (Rel.
                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                 Allochromatium.
NCBI_TaxID=1049;
                                                                                                                                                                                                                                      Cusanovich M.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             62;
         ANKH CHRVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
         δ
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                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation. The Suropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         64 VRKTSLDLRREIIDVGGIQNLIE-----LRKKRKQKKRD--ALAASHEPPPEPEEITG 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             201 ------LLQSHGADTNVRDKLLSTPLHVAVRTGQVEIVEHFLSL-GLEINAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               210 LLSSDDSDVEAITHLLLDHGADVNVRGERGKTPLILAVEKKHLGLVQRLLEQEHIEINDT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       115 PVDEETFLKAAVEGKMKVIEKFLADGGSADTCDQFRRTALHRASLEGHMEILEKLLDNGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           246 DREGDTALHDAVRLINRYKIIKLLLLHGADMMTKNLAGKTPTDLVQLWQADTRHALE----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     86;
                                                                                                                                                                                                                                         InterPro; IPR002110; ANK.
InterPro; IPR002110; Buk_pkinase,
Pfam; PF00023; ank; 8.
SMART; SM00248; ANK; 8.
PROSITE; PS50088; ANK; B.
PROSITE; PS5011; ANK REP_REGION; 1.
PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
Hydrolase; Nuclease; RNA-binding; Endonuclease; Zinc-finger;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 741;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                42; Mismatches 110; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -TYPE (POTENTIAL).
91385EA307E3CEID CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROTEIN KINASE LIKE.
2-5A BINDING (P-LOOP) 1.
2-5A BINDING (P-LOOP) 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  175 TVDF-----QDRL---DCTAMHWACRGGHLEVVK-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12.8%; Score 217; DB 1; 26.3%; Pred. No. 9.8e-08;
EITHER MANGANESE OR MAGNESIUM AND ATP
                             !- INDUCTION: BY INTERFERON.
!- SIMILARITY: CONTAINS 9 ANK REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  ANK 4.
ANK 5.
ANK 6.
ANK 7.
ANK 8.
                                                                                                                                                                                                                                                                                                                                                                                                        35.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          322 SHGAKEDFHPPAEDWKPQSSHWG 344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     83532 MW;
                                                                                                                                                                                                    EMBL; L10381; AAA18032.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 12.89
Best Local Similarity 26.39
Matches 85; Conservative
                                                                                                                                                                                                                    Q00420; 1AWC.
                                                                                                                                                                                                                                                                                                                                                                                    Repeat; ANK repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       395
741 AA:
                                                                                                                                                                                                                                 MIM; 180435;
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SEQUENCE
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235 FLSLGLEINARDREGDTALHDAVRLNRYKIIKLLLLHGADMMTKNLAGKTP 285
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      175 TVDFQDRLDCTAMHWACRGGHLEVVKLLQSHGADTNVRDKLLSTPLHVAVRTGQVEIVEH 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              124 AAVEGKMKVIEKFLADGGSA-----DTCDQFRRTALHRASLEGHMEILEKLLDN-GA 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10; Gaps
                                                                                                        Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                               STRAIN=BRISTOL N2;
MEDLINE=90199879; PubMed=2317869;
Spence A.M., Coulson A., Hodgkin J.;
The product of fem-1, a nematode sex-determining gene, contains a found in cell cycle control proteins and receptors for
                                                                                                                                                                                                                                                                               Submitted (MAR-1996) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: SEX-DETERMINING PROTEIN. IT IS ESSENTIAL FOR THE
ADOPTION OF THE MALE SEXUAL FATE IN ALL TISSUES IN C.ELEGANS.
-!- SUBCELLULAR LOCATION: CYTOPLASMIC (POTENTIAL).
-!- SIMILARITY: CONTAINS 7 ANK REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Developmental protein; Phosphorylation; ANK repeat; Repeat. REPEAT 47\ 76\ {\rm ANK}\ 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 656;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    75; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4F5FC3FA3EA950D3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 212; DB 1;
Pred. No. 1.9e-07;
                                           (Rel. 15, Created)
(Rel. 15, Last sequence update)
(Rel. 40, Last annotation update)
                        656 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SMART; SM00248; ANK; 5.
PROSITE; PS50088; ANK_REPEAT; 4.
PROSITE; PS50297; ANK_REP_REGION; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ANK 3.
ANK 4.
ANK 5.
ANK 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 74286 MW;
                                                                           SEX-DETERMINING PROTEIN FEM-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12.5%;
32.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; J03172; AAA28055.1; -. EMBL; U52001; AAA96093.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WormPep; F35D6.1; CE07175.
InterPro; IPR002110; ANK.
Pfam; PF00023; ank; 8.
SMART; SM00248; ANK; 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 32.78
                                                                                     FEM-1 OR ISX-1 OR F35D6.1.
                                                                                                                                                                                                                    cell-cell interactions."; cell 60:981-990(1990).
                        STANDARD;
                                                                                                Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         PIR; A34793; A34793
HSSP; Q00420; 1AWC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      155
188
220
557
656 AA;
                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. STRAIN-BRISTOL N2;
                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                         Waterston R.;
                                            01-AUG-1990
                                                     01-AUG-1990
20-AUG-2001
                      FEM1_CAEEL P17221;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REPEAT
SEQUENCE
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REPEAT
REPEAT
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REPEAT
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   RESULT 11
              FEM1_CAEEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      heterodimer bound to DNA.";
Science 279:1037-1041(1998).
-!- FUNCTION: TRANSCRIPTION FACTOR CAPABLE OF INTERACTING WITH PURINE
RICH REPEATS (GA REPEATS).
                                                                                                                                                                                                                                                                                                                                                                                       Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PIR; C40858; C40858.
PDB; 1AWC; 18-MAR-98.
TRANSFAC; T00209; -
TRANSFAC; T01404; -
MGD; MGI:95611; Gabpl.
InterPo: 1PR0023; ank; 3.
SMART; SM00248; ANK_REPEAT; 3.
PROSITE; PS50098; ANK_REP_REGION; 1.
Transcription regulation; Nuclear protein; Alternative splicing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lamarco K., Thompson C.C., Byers B.P., Walton E.M., McKnight S.L. Identification of Ets- and notch-related subunits in GA binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -!- SUBUNIT: HETEROTETRAMER OF TWO ALPHA AND TWO BETA SUBUNITS.
-!- ALTERNATIVE PRODUCTS: THE BETA-1 AND BETA-2 SUBUNITS ARE PRODUCED BY ALTERNATIVE SPLICING OF THE SAME GENE AND ONLY DIFFER IN THEIR C-TERNAINAL EXTREMITY.
-!- SIMILARITY: CONTAINS 5 ANK REPEATS.
                                                                                                                                                                                                                    01-DEC-1992 (Rel. 24, Created)
01-DEC-1992 (Rel. 24, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
GA BINDING PROTEIN BETA-2 CHAIN (GABP-BETA-2 SUBUNIT) (GABBP2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "The structure of GABPalpha/beta: an ETS domain-ankyrin repeat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Batchelor A.H., Piper D.E., de la Brousse F.C., McKnight S.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 347;
175 LLKTGIDVNKKTERGNTALHDAAESGNVEVVKILLKHGSVLM-KDIQGVDP 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -> VV (IN REF. 1; AAA53032)
01D6AB96BBB83D05 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 208.5; DB 1;
Pred. No. 1.4e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           X-RAY CRYSTALLOGRAPHY (2.15 ANGSTROMS) OF 5-157.
                                                                                                                                                               347 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ANK 4.
                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=91343912; PubMed=1876836;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-98128030; PubMed-9461436;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3D-structure
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               36867 MW;
                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rođentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; M74517; AAA53032.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12.3%;
27.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Science 253:789-792(1991).
                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                     Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                        GABPB1 OR GABPB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Wolberger C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ANK repeat;
                                                                                                                                                                  GABC_MOUSE
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                                                                                           195 HLEVVKLLQSHGADTNVRDKLLSTPLHVAVRTGQVEIVEHF-LSLGLEINARDREGDTAL 253
                                                                                                                                             75 IIDVGGIQNLIELRKKRKQKKRDALAASHEPPPEPEEITGPVDEETFLKAAVEGKMKVIE 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -i- FUNCTION: TRANSCRIPTION FACTOR CAPABLE OF INTERACTING WITH PURINE RICH REPEATS (GA REPEATS).
-i- SUBUNIT: HETEROTETRAMER OF TWO ALPHA AND TWO BETA SUBUNITS.
        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-91343912; PubMed-1876836;
Lamarco K., Thompson C.C., Byers B.P., Walton E.M., McKnight S.L.;
"Identification of Ets- and notch-related subunits in GA binding
                                          135 KFLADGGSADTCDQFRRTALHRASLEGHMEILEKLLDNGATVDFQDRLDCTAMHWACRGG
                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBL_TaxID=10090;
        31;
                                                                                                                                                                                                                                                                                             01-DEC-1992 (Rel. 24, Created)
01-DEC-1992 (Rel. 24, Last sequence update)
01-DEC-2001 (Rel. 40, Last annotation update)
GA BINDING PROTEIN BETA-1 CHAIN (GABP-BETA-1 SUBUNIT) (GABPB1).
GABPBI OR GABPB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ALTERNATIVE PRODUCTS: THE BETA-1 AND BETA-2 SUBUNITS ARE PRODUCED BY ALTERNATIVE SPLICING OF THE SAME GENE AND ONLY DIFFER IN THEIR C-TERMINAL EXTREMITY.
SIMILARITY: CONTAINS 5 ANK REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "The structure of GABPalpha/beta: an ETS domain-ankyrin repeat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Batchelor A.H., Piper D.E., de la Brousse F.C., McKnight S.L.,
                                                                                                                                                                               254 HDAVRLNRYKIIKLLLLHGADMM-----TKNLAGKTPTDLVQLWQADT 296
                                                                                                                                                                                                    174 -----VIIHAATPQFIIGPGGVVNLTDETGVSAVOFGNSST 209
    34; Mismatches 101; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                X-RAY CRYSTALLOGRAPHY (2.15 ANGSTROMS) OF 5-157. MEDLINE-98128030; PubMed=9461436;
                                                                                                                                                                                                                                                                          382 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR002110; ANK.
Pfam; PF00023; ank; 3.
SMART; SM00248; ANK, 3.
PROSITE; PS50088; ANK_REPEAT; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; M74516; AAA53031.1; -. PIR; B40858; B40858.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              heterodimer bound to DNA.";
Science 279:1037-1041(1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Science 253:789-792(1991).
  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MGD; MGI:95611; Gabpbl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PDB; 1AWC; 18-MAR-98.
TRANSFAC; T00298; -.
TRANSFAC; T01403; -.
                                                                                                                                                                                                                                                                                                                                                             Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
64;
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GABB_MOUSE
ID GABB_MOUSE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HLEVVKLLQSHGADTNVRDKLLSTPLHVAVRTGQVEIVEHF-LSLGLEINARDREGDTAL 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              notch motifs.";
Mol. Cell. Biol. 13:1385-1391(1993).
-!- FUNCTION: TRANSCRIPTION FACTOR CAPABLE OF INTERACTING WITH PURINE RICH REPEATS (GA REPEATS). NECESSARY FOR THE EXPRESSION OF THE ADENOVIRUS E4 GENE.
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01-NOV-1995 (Rel. 32, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
GA BINDING PROTEIN BETA-2 CHAIN (GABP-BETA-2 SUBUNIT) (TRANSCRIPTION
                                                                                                                                                                                                                                                                                                                                                                                                                               3 LVDLG--KKLLEAARAGODDEVRILMANGAPFTTDWLGTSPLH-----LAAQYGHFSTTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                135 KFLADGGSADTCDQFRRTALHRASLEGHMEILEKLLDNGATVDFQDRLDCTAMHWACRGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "CDNA cloning of transcription factor E4TF1 subunits with Ets and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chordata; Craniata; Vertebrata; Euteleostomi; Primates; Catarrhini; Hominidae; Homo.
PROSITE; PS50297; ANK_REP_REGION; 1.
Transcription regulation; Nuclear protein; Alternative splicing;
                                                                                                                                                                                                                                                                                                                                      31;
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ALTERNATIVE PRODUCTS: THE BETA-1 AND BETA-2 SUBUNITS ARE
PRODUCED BY ALTERNATIVE SPLICING OF THE SAME GENE AND ONLY
DIFFER IN THEIR C-TERMINAL EXTREMITY.
SIMILARITY: CONTAINS 5 ANK REPEATS.
                                                                                                                                                                                                                                                                                    Length 382;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
MEDLINE-93180783; Pubmed-8441384;
Watanabe H., Sawada J.-I., Yano K.-I., Yamaguchi K., Goto M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           174 ------VTIHAATPQFIIGPGGVVNLTDETGVSAVQFGNSST 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               254 HDAVRLNRYKIIKLLLLHGADMM-----TKNLAGKTPTDLVQLWQADT 296
                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                      0A5FE3F71D4227AF CRC64;
                                                                                                                                                                                                                                                                                    DB 1;
                                                                                                                                                                                                                                                                                                                                   101;
                                                                                                                                                                                                                                                                            12.3%; Score 208.5; DB 27.8%; Pred. No. 1.6e-07;
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                                                                                                                                                                                                                                                                                                                                   34; Mismatches
                                                                         ANK 1.
ANK 2.
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                                                                                                                                                                              ANK
                                                    ANK repeat; 30-structure REPEAT 5
                                                                                                                                                                                                      41,258 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FACTOR E4TF1-47) (GAPBP2). GABPB1 OR GABPB OR E4TF1B.
                                                                                                                                                                                                                                                                                                                              64; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
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                                                                                                                                                                                                   382 AA;
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70
103
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Q06545;
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Search completed: April 17, 2002, 08:13:23 Job time: 181 sec
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**MEDLINE=95097980; PubMed=7799916;

Gugneja S., Virbasius J.V., Scarpulla R.C.;

Gugneja S., Virbasius J.V., Scarpulla R.C.;

"Four structurally distinct, non-DNA-binding subunits of human nuclear respiratory factor 2 share a conserved transcriptional activation domain."; Data of the second of the ROTOR REPEATS (GA REPEATS). NECESSARY FOR THE EXPRESSION OF THE ADENOVIRUS E4 GENE.

-1- SUBUNIT: HETEROTETRAMER OF TWO ALPHA AND TWO BETA SUBUNITS.
                                                                                                                                                                                                                                                                                                                                    56 VILRAGVSRDARTKVDRTPLHMAASEGHASIVEVLLKHGADVNAKDMLKMTALHWATEHN 115
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                                                                                                                                                                                                                                                                                                                                                                                       75 IIDVGGIQNLIELRKKRKKKKRDALAASHEPPPEPEEITGPVDEETFLKAAVEGKMKVIE 134
                                                                                                                                                                                                                                                                                                                      135 KFLADGGSADTCDQFRRTALHRASLEGHMEILEKLLDNGATVDFQDRLDCTAMHWACRGG 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-NOV-1995 (Rel. 32, Last sequence update)
20-AGG-2001 (Rel. 40, Last annotation update)
40-AGG-2001 (Rel. 40, Last annotation update)
50-BINDING PROTEIN BETA-1 CHAIN (GABP-BETA-1 SUBUNIT) (TRANSCRIPTION FACTOR E4FF1-53) (GABPB1) (NUCLEAR RESPIRATORY FACTOR-2 SUBUNIT BETA
                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                    Homo sapiens (Human).
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Pinmates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cDNA cloning of transcription factor E4TF1 subunits with Ets and
                 MIN; 9006LU;
InterPro; IPR002110; ANK.
Pfam; PF000023; ank; 3.
SMART; SM00248; ANK; 3.
PROSITE; PS50088; ANK_REPEAT; 3.
PROSITE; PS50297; ANK_REP_REGION; 1.
Transcription regulation; Nuclear protein; Alternative splicing;
                                                                                                                                                                                                                                            31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-93180783; PubMed-8441384;
Watanabe H., Sawada J.-I., Yano K.-I., Yamaguchi K., Goto M.,
                                                                                                                                                                                                                Length 347;
                                                                                                                                                                                                                                                                                                                                                                                                                          254 HDAVRLNRYKIIKLLLHGADMM-----TKNLAGKTPTDLVQLWQADT 296
                                                                                                                                                                                                                                                                                                                                                                                                                                          174 ------VTIHAATPQFIIGPGGVVNLTDETGVSAVQFGNSST 209
                                                                                                                                                                                                                 12.3%; Score 207.5; DB 1; Length 27.8%; Pred. No. 1.7e-07; Live 34; Mismatches 101; Indels
                                                                                                                                                                             902C02A3F6ABBA2E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               383 AA
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                                                                                                                                                                             36850 MW;
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                                                                                                                                                                                                                                             Conservative
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TRANSFAC; T01392; -.
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                                                                                                     Repeat
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Best Local Similarity
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103
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01-NOV-1995
20-AUG-2001
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             MIM; 600610;
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REPEAT
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Q06547;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            75 IIDVGGIQNLIELRKKRKQKKRDALAASHEPPPEPEEITGPVDEETFLKAAVEGKMKVIE 134
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                                                                                                                                                                                                                                                                                                                                                                  Pfem; PF00023; ank; 3.
SMART; SM00248; ANK; 3.
PROSITE; PS50088; ANK_REPEAT; 3.
PROSITE; PS50247; ANK_REP_REGION; 1.
Transcription regulation; Nuclear protein; Alternative splicing; ANK repeat; Repeat.
5 34 ANK 1
-i- ALTERNATIVE PRODUCTS: THE BETA-1 AND BETA-2 SUBUNITS ARE PRODUCED BY ALTERNATIVE SPLICING OF THE SAME GENE AND ONLY DIFFER IN THEIR C.TERMINAL EXTREMITY.
-i- SIMILARITY: CONTAINS 5 ANK REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 383;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 254 HDAVRLNRYKIIKLLLHGADMM-----TKNLAGKTPTDLVQLWQADT 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ------VIIHAATPOFIIGPGGVVNLTDETGVSAVQFGNSST 209
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ANK 2.

ANK 3.

ANK 4.

ANK 4.

O7E7081A60016288 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12.3%; Score 207.5; DB 1; 27.8%; Pred. No. 1.9e-07;
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InterPro; IPR002110; ANK.
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383 AA;
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TRANSFAC; T01391;
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Best Local 3
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Patent No. 6277613

GENERAL INFORMATION:
APPLICANT: General APPLICANT: Smith, Susan
TITLE OF INVENTION: A PROTEIN THAT BINDS TO TRF1 AND METHODS
TITLE OF INVENTION: OF USE THEREOF
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
ADDRESSEE: 411 Hackensack Avenue, 4th Floor
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/196,387
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14.7%; Score 249.5; DB 4; 26.2%; Pred. No. 3.4e-16; ive 33; Mismatches 110;
                                            US-08-701-005A-2

US-08-479-895-2

US-08-479-895-2

PCT-US95-02058-4

US-09-031-485-33

US-08-847-424A-33

US-08-847-424A-33

US-08-810-712-10

US-08-996-485-3

US-09-055-474-139

US-09-031-485-20

US-09-031-425A-20

US-09-065-474-10

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REFERENCE/DOCKET NUMBER: 600-1-230 CIP1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
TELEFAX: 201-343-1684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/095,225
FILING DATE: June 10, 1998
ATTORNEY/AGENT INFORMATION:
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LENGTH: 949 amino acids
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TELEX: 133521
INFORMATION FOR SEQ ID NO:
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; MOLECULE TYPE: protein US-09-196-387-10
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STATE: New Jersey
COUNTRY: USA
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Best Local Similarity
Matches 91; Conserv
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/cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PcTUS_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PcTUS_COMB.pep:*
                        GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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US-09-172-977-3
US-09-082-059-2
US-08-436-771-6
US-08-437-998-6
US-08-477-998-6
US-08-771-6
US-08-771-6
US-08-779-6
US-08-77-95-6
US-08-77-9-85-6
US-08-479-869-6
US-08-486-414-6
PCT-US94-01826A-6
US-08-943-956A-4
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US-08-943-956A-2
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US-08-434-998-4
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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length: 2000000000
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Match Length DB
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Sequence:
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Maximum DB seq
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636 QQILSESTPIRTSDVDYRLLEASKAGDLETVKQLCSSQNVNCRDLEGRHSTPLHFAAGYN 695
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                     ---KKRDALAASHEPPPEPEITGPVDEETFLKAAVEGKMKVIE 134
                                                                                                                                                                                                                                               195 HLEVVKLLQSHGADTNVRDKLLSTPLHVAVRTGQVEIVEHFLSLGLEINARDREGDTALH 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: de Lange, Titia
APPLICANT: Smith, Susan
TITLE OF INVENTION: A PROTEIN THAT BINDS TO TRF1 AND METHODS
TITLE OF INVENTION: OF USE THEREOF
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                           255 DAVRLNRYKIIKLLLLHGADMMTKNLAGKTPTDLVQLWQADTRHALE 301
LVLEDEKH----HGAQSAALQKVKGQERVRKTSLDLRREIIDVGGIQN-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/196,387
                                                                            135 KFLADGGSADTCDQFRRTALHRASLEGHMEILEKLLDNG---
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411 Hackensack Avenue, 4th Floor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               09/095,225
                                                                                                                                                                                                                                                                                                                                                                                                     US-09-196-387-2; Sequence 2, Application US/09196387; Patent No. 6277613
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/095,
FILING DATE: June 10, 1998
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: 60
TELECOMMUNICATION:
TELEPHONE: 201-487-5800
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INFORMATION FOR SEQ ID NO:
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New Jersey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hackensack
                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRANDEDNESS:
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, HYPOTHETICAL:
US-09-196-387-2
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636 QQILSESTPIRTSDVDYRLLEASKAGDLETVKQLCSSQNVNCRDLEGRH9TPLHFAAGYN 695
                                                                                                  -KKRDALAASHEPPPEPEEITGPVDEETFLKAAVEGKMKVIE 134
                                                                                                                                                                                                                                                                                                    ----DRLDC-----TAMHWACRGG 194
                                                                                                                                                                                                                                                                                                                                                                          195 HLEVVKLLQSHGADTNVRDKLLSTPLHVAVRTGQVEIVEHFLSLGLEINARDREGDTALH 254
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   Length 1327;
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                                                                            40 LVLEDEKH---HGAQSAALQKVKGQERVRKTSLDLRREIIDVGGIQN----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 4, Application US/09172977

Patent No. 5989863

GENERAL INFORMATION:
APPLICANT: Tang, Y. Tom
APPLICANT: Guegler, Karl J.
APPLICANT: Corley, Neil C.
APPLICANT: Corley, Neil C.
TITLE OF INVENTION: HUMAN ANKYRIN FAMILY PROTEIN
FILE REFERENCE: PF-0615 US
CURRENT APPLICATION UNUMBER: US/09/172,977
CURRENT FILING DATE: 1998-10-14
NUMBER OF SEQ ID NOS: 4
SOFTWARE: PERL PROGRAM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 --RHALEHPEPGAEHNGLEGPNDSGRET 322
                                                                                                                                                                              13.9%; Score 234.5; DB 2; 29.5%; Pred. No. 2.7e-14; cive 32; Mismatches 100;
14.7%; Score 249.5; DB 4; 26.2%; Pred. No. 5.6e-16; ive 33; Mismatches 110;
                                                                                                                                                                                                                             135 KFLADGGSADTCDQFRRTALHRASLEGHMEILEKLLDNG----
                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 29.54
Matches 65; Conservative
                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ) OTHER INFORMATION: 929491
US-09-172-977-4
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                       Similarity
                                                                                                                                                      89 KKRKQ--
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                                           91;
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US-09-172-977-4
   Query Match
Best Local S
Matches 91
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13;
                                                                184 CTAMHWACRGGHLEVVKLLQSHGADTNVRDKLLSTPLHVAVRTGQVEIVEHFLSLGLEIN 243
                                                                                                 88 ETALHWAARSGQAEVVRYLVQDGAQVEAKAKDDQTPLHISARLGKADIVQQLLQQGASPN 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         94 KKRDA--LAASHEPPPEPEEITGPVDEETFLKAAVEGKMKVIEKFLADGGSADTCDQ--- 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ---FRR-----TALHRASLEGHMEILEK 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28 ACKKNRIKVMELLIKHGASIQAVTESGLTPIHVAAFMGHVNIVSQLMHHGASPNTTNVRG 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               41 VLEDEKHHGAQSAALQKVKGQERVRKTSLDLRREIIDVGGIQNLIE-----LRKKRKQ 93
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ruden, Barnett, McClosky, Smith, Schuster & Russell
                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Silverman, Robert H.
APPLICANT: Hassel, Bret A.
APPLICANT: Zhou, Aimin
TITLE OF INVENTION: Animal 2-5A- Dependent RNases and
TITLE OF INVENTION: Encoding Sequence Therefor
                                                                                                                                                                                  244 ARDREGDTALHDAVRLNRYKIIKLLLLHGADMMTKNLAGKTP 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/462,481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    41; Mismatches 101;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13.2%; Score 224; DB 2; 28.1%; Pred. No. 7.3e-14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: 200 East Broward Boulevard
CITY: Fort Lauderdale
CTATE: Florida
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/028,086
FILING DATE: 08-WAR-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                 Sequence 4, Application US/08462481 Patent No. 5840577 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       32,264
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REGISTRATION NUMBER: 32,260
REFERENCE/DOCKET NUMBER: CI
TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         679 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 305/764/4996
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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Matches 89; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; MOLECULE TYPE: protein US-08-462-481-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 33301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: Ruden, Ba
ADDRESSEE: Russell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Patent No. 5840577
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 amino acid
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                                                                                                                                                                                                                                                                          RESULT 6
US-08-462-481-4
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APPLICANT: MOSTOW, Jon S.

APPLICANT: MOSTOW, Jon S.

APPLICANT: MOSTOW, Jon S.

TITLE OF INVENTION: No. 6225086e1 Ankyrin Proteins and a Method for Their Identificat FILE REFERENCE: 44574-5002-US

CURRENT APPLICATION NUMBER: 05/09/082,059A

CURRENT FLING DATE: 1998-05-21

EARLIER APPLICATION NUMBER: 60/047356

EARLIER FILING DATE: 1997-05-21

NUMBER OF SEQ ID NOS: 19

SOFTWARE: Patentin Ver. 2.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           124 AAVEGKMKVIEKFLADGGSADTCDOFRRTALHRASLEGHMEILEKLLDNGATVDFQDRLD 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           601 AAKKNQMQIASTLLNYGAETNTVTKQGVTPLHLASQEGHTDMVTLVLEKGANIHMSTKSG 660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         184 CTAMHWACRGGHLEVVKLLQSHGADTNVRDKLLSTPLHVAVRTGQVEIVEHFLSLGLEIN 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 244 ARDREGDTALHDAVRLNRYKIIKLLLLHGADMMTKNLAGKTPTDLVQ----LWQADT--- 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 124 AAVEGKMKVIEKFLADGGSADTCDQFRRTALHRASLEGHMEILEKLLDNGATVDFQDRLD 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 13.7%; Score 231.5; DB 2; Best Local Similarity 29.1%; Pred. No. 1.8e-14; Matches 64; Conservative 33; Mismatches 100;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 13.5%; Score 228; DB 4; 1
Best Local Similarity 33.3%; Pred. No. 5.7e-14;
Matches 54; Conservative 26; Mismatches 82;
                                                                                                      GENERAL INFORMATION:
APPLICANT: Tang, Y. Tom
APPLICANT: Tang, Y. Tom
APPLICANT: Guegler, Karl J.
APPLICANT: Corley, Neil C.
APPLICANT: Yue, Henry
APPLICANT: Yue, Henry
FITLE OF INVENTION: HUMAN ANKYRIN FAMILY PROTEIN
FILE REFERENCE: PF-0615 US
                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/09/172,977
CURRENT FILING DATE: 1998-10-14
NUMBER OF SEQ ID NOS: 4
SOFTWARE: PERL Program
SEQ ID NO 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 2, Application US/09082059A Patent No. 6225086
                                                           Sequence 3, Application US/09172977
Patent No. 5989863
                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ) OTHER INFORMATION: 91841966
US-09-172-977-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; ORGANISM: Homo sapiens
US-09-082-059-2
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LENGTH: 1088
                                                                                                                                                                                                                                                                                                                                                                                      843
                                          US-09-172-977-3
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LL-DNGATVDFQDR----LDCTAMHWACRGGHLEVVKLLQSHGADTNVRDKLLSTPLHV 222
                                                                                                                                 187 LLNDMKAEVDARDNMGRNALIRTLLNWDCENVE-BITSILIQHGADVNVRGERGKTPLIA 245
                                                                                                                                                                            223 AVRTGQVEIVEHFLSL-GLEINARDREGDTALHDAVRLNRYKIIKLLLLHGADMMTKNLA 281
                                                                                                                                                                                                     94 KKRDA--LAASHEPPPEPEEITGPVDEETFLKAAVEGKMKVIEKFLADGGSADTCDQ--- 148
                                                     127 TAFMEAAERGNAEALRFLFAKGANVNLRRQTTKDKRRLKQGGATALMSAAEKGHLEVLRI 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          41 VLEDEKHHGAQSAALQKVKGQERVRKTSLDLRREIIDVGGIQNLIE-----LRKKRKQ 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22 VVEDD-----SSLIKAVQKGDVVRV-----QQLLEKGADANACEDTWGWTPLHNAVQA 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Silverman, Robert H.
APPLICANT: Sengupta, Dibyendu N.
TITLE OF INVENTION: Antiviral Transgenic Plants, Vectors, TITLE OF INVENTION: Cells and Methods
NUM.JER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Ruden, Barnett, McClosky, Smith, Schuster ADDRESSEE: Russell STREET: 200 E. Broward Boulevard STREET: Ruderdale STATE: Florida
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    41; Mismatches 101;
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Pred. No. 7.3e-14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US 08/198,973
FILING DATE: 18-FEB-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US/08/434,998
                                                                                                                                                                                                                                                                                                                                                                                        US-08-434-998-6; Sequence 6, Application US/08434998; Patent No. 5866781
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REGISTRATION NUMBER: 32,264
REFERENCE/DOCKET NUMBER: CI
TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13.2%;
ilarity 28.1%;
Conservative 4
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MEDIUM TYPE: Floppy disk
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amino acid
                                                                                                                                                                                                                                                                  282 GKTPTDLVQLWQADTRH 298
                                                                                                                                                                                                                                                                                                        301 ---- DDLV--WIARRNH 311
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     305/764/4996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; MOLECULE TYPE: protein US-08-434-998-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 89; Conservi
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                 149
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               --LDCTAMHWACRGGHLEVVKLLQSHGADTNVRDKLLSTPLHV 222
                                                                                   AVRTGOVEIVEHFLSL-GLEINARDREGDTALHDAVRLNRYKIIKLLLLHGADMMTKNLA 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22 VVEDD-----SSLIKAVQKGDVVRV-----QQLLEKGADANACEDTWGWTPLHNAVQA 69
                                                                                                                                                                   ; DB 2; Length 679; 7.3e-14;
                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Silverman, Robert H.
APPLICANT: Salverman, Dibyendu N.
TITLE OF INVENTION: Antiviral Transgenic Plants, Vectors,
TITLE OF INVENTION: Cells and Methods
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Ruden, Barnett, McClosky, Smith, Schuster
ADDRESSEE: Russell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        41 VLEDEKHHGAQSAALQKVKGQERVRKTSLDLRREIIDVGGIQNLIE---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Lam PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               41; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: CL11363-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 536 .
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/198,973
FILING DATE: 18-FEB-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: 200 E. Broward Boulevard
CITY: Fort Lauderdale
STATE: Florida
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/08/436,777 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                       Sequence 6, Application US/08436771
Patent No. 5861300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                             282 GKTPTDLVQLWQADTRH 298
                                                                                                                                                                                                                                                                  ----DDLV--WIARRNH 311
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; MOLECULE TYPE: protein US-08-436-771-6
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REGISTRATION NUMBER:
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-TALHRASLEGHMEILEK 168
                                                                                                                   127 TAFMEAAERGNAEALRFLFAKGANVNLRRQTTKDKRRLKQGGATALMSAAEKGHLEVLRI 186
                                                                                                                                                                                                169 LL-DNGATVDFQDR----LDCTAMHWACRGGHLEVVKLLQSHGADTNVRDKLLSTPLHV 222
                                                                                                                                                                                                                                                                        187 LLNDMKAEVDARDNMGRNALIRTLLNWDCENVE-EITSILIQHGADVNVRGERGKTPLIA 245
                                                                                                                                                                                                                                                                                                                                                                                                    223 AVRTGQVEIVEHFLSL-GLEINARDREGDTALHDAVRLNRYKIIKLLLLHGADMMTKNLA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: Animal 2-5A-Dependent RNases and TITLE OF INVENTION: Encoding Sequence Therefor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Pred. No. 7.3e-14; 41; Mismatches 101;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Rothwell, Figg, Ernst & Kurz
STREET: 555 - 13th Street, N.W., Suite 701
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/141,304
FILING DATE: 22-OCT-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/028,086
FILING DATE: 08 WAR-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           UMBER: US/08/701,005A
21-AUG-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 4, Application US/08701005A
Patent No. 5877019
GENERAL INFORMATION:
APPLICANT: Silverman, Robert H.
APPLICANT: Hassel, Bret A.
APPLICANT: Zhou, Aimin
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-783-6040
TELEFAX: 202-783-6031
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              679 amino acids
amino acid
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Best Local Similarity 28.15
Matches 89; Conservative
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NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
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ZIP: 20004
COMPUTER READABLE FORM:
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                                                                                                                                                                  94 KKRDA--LAASHEPPPEFPEITGPVDEETFLKAAVEGKMKVIEKFLADGGSADTCDQ--- 148
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                                                                                                                   ---TALHRASLEGHMEILEK 168
                                                                                                                                                                                                                                                                             LL-DNGATVDFQDR-----LDCTAMHWACRGGHLEVVKLLQSHGADTNVRDKLLSTPLHV 222
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                                                                                                                                                                                                                                                                                                                                                                                                                                               223 AVRTGQVEIVEHFLSL-GLEINARDREGDTALHDAVRLNRYKIIKLLLLHGADMMTKNLA
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APPLICANT: Silverman, Robert H.
APPLICANT: SenGupta, Dibyendu N.
TITLE OF INVENTION: Transgenic Plants Co-Expressing A
TITLE OF INVENTION: Functional Human 2-5A System
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,797
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41; Mismatches 101;
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                                                                                                                       ------FRR-----
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ZIP: 33301
COMPUTER REABLE FORM:
MEDIUM TYPE: Floppy disk
"COMPUTER: IBM PC COMPATIBLE
"COMPATIENTER: TEM PC COMPATIBLE
"CO
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Patent No. 5866787
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REGISTRATION NUMBER: 32,264
REFERENCE/DOCKET NUMBER: CL
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amino acid
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ADDRESSEE: Holland &
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Matches 89; Conserv
                                                                                                                   149 -----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY:
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70 GRVDIVNLLESHGADPHRRKKNGAT---PFIIAGIQGDVKLLEILLSCGADVNECDENGF 126
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                                                                                                                                                                                                                                                                                           223 AVRTGQVEIVEHFLSL-GLEINARDREGDTALHDAVRLNRYKIIKLLLLHGADMMTKNLA 281
94 KKRDA--LAASHEPPPEPEEITGPVDEETFLKAAVEGKMKVIEKFLADGGSADTCDQ---
                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSEE: Ruden, Barnett, McClosky, Smith, Schuster & ADDRESSEE: Russell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 4, Application US/08479895
Patent No. 5972678
Patent No. 5972678
GENERAL INFORMATION:
APPLICANT: Bilverman, Robert H.
APPLICANT: Hassel, Bret A.
APPLICANT: Anou, Animin
TITLE OF INVENTION: Animal 2-5A- Dependent RNases and
TITLE OF INVENTION: Encoding Sequence Therefor
Patent No. 5972678
NUMBER OF SEQUENCES: 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN RELEASE #1.0, VETSION #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/479,895
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CL11363-13
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CITY: Fort Lauderdale
STATE: Florida
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/028,086
FILING DATE: 08-MAR-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Manso, Peter J
REGISTRATION NUMBER: 32,264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: CL
TELECOMMUNICATION INFORMATION:
TELEPHONE: 305/527/2498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: 4: SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                         ----DDLV--WIARRNH 311
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Length 679;

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13.2%; Score 224;

Query Match

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                                                                                                                                         94 KKRDA--LAASHEPPPEPEEITGPVDEETFLKAAVEGKMKVIEKFLADGGSADTCDQ--- 148
                                                                                                                                                                       O GRVDIVNLLLSHGADPHRRKKNGAT---PFIIAGIQGDVKLLEILLSCGADVNECDENGF 126
                                                                                                                                                                                                                            ---FRR-------TALHRASLEGHMEILEK 168
                                                                                                                                                                                                                                                 86; Gaps
                                                                                               22 VVEDD-----SLIKAVQKGDVVRV-----QULLEKGADANACEDTWGWTPLHNAVQA 69
                                                           41 VLEDEKHHGAQSAALQKVKGQERVRKTSLDLRREIIDVGGIQNLIE-----LRKKRKQ 93
                                                                                                                                                                                                                                                                                                       LL-DNGATVDFQDR-----LDCTAMHWACRGGHLEVVKLLQSHGADTNVRDKLLSTPLHV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Silverman, Robert H.
APPLICANT: SenGupta, Dibyendu N.
TITLE OF INVENTION: Antiviral Transgenic Plants, Vectors, TITLE OF INVENTION: Cells and Methods
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
Best Local Similarity 28.1%; Pred. No. 7.3e-14;
Matches 89; Conservative 41; Mismatches 101; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Ruden, Barnett, McClosky, Smith, Schuster
ADDRESSEE: Russell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/02058
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/198,973
FILING DATE: 18-FEB-1994
ATTORNEY/AGENT INFORMATION:
NAME: Manso, Peter J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               200 E. Broward Boulevard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 6, Application PC/TUS9502058 GENERAL INFORMATION:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        301 ----DDLV--WIARRNH 311
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305/764/4996
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; MOLECULE TYPE: protein
PCT-US95-02058-6
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44 RTGNAKIVELFIKHGAQVNHVNTKIPNPLLTAIKIGSHDIVKLLLINGVDTSILPVPCIN 103
                                                                                                                                    223 AVRTGQVEIVEHFLSLGLEINARDREGDTALHDAVRLNRYKIIKLLLLLHGADMMTKNLAG 282
                                                                                                                                                                                                                163 MEILEKLLDNGATVDFQDRLDCTAMHWACRGGHLEVVKLLQSHGADTNVRDKLLSTPLHV 222
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     44 RTGNAKIVELFIKHGAQVNHVNTKIPNPLLTAIKIGSHDIVKLLLINGVDTSILPVPCIN 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           163 MEILEKLLDNGATVDFQDRLDCTAMHWACRGGHLEVVKLLQSHGADTNVRDKLLSTPLHV 222
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  ---KNKGNCINIS-----VEETTTPL----IDAI 43
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Recombinant Fowlpox Viruses and Uses
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                98; Indels
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25.9%; Pred. No. 4.6e-14;
Live 48; Mismatches 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 126 VEGKMKVIEKFLADGGSADTCD-QFRRTALHRASLEGH--
                                    126 VEGKMKVIEKFLADGGSADTCD-QFRRTALHRASLEGH-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                E: John P. White
1185 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 6, Application US/08477459
Patent No. 6001369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: White Esq. John P
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Mark D. Cochran
TITLE OF INVENTION: Recombin:
TITLE OF INVENTION: Thereof
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: (212) 278-0400
TELEFAX: (212) 391-0525
INFORMATION FOR SEQ ID NO: 6:
                                                                                                                                                                                                                                                                                          224 VTPLHNAILY---NRSAVE 239
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  2 SVDWRTEIYSGDISLVEKLI---
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amino acid
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Best Local Similarity 25.9
Matches 67; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; MOLECULE TYPE: protein US-08-477-459-6
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: 1185 AV....
CITY: New York
STATE: New York
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US-08-477-459-6
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                                      13;
                                                                                                                                                  94 KKRDA--LAASHEPPPEPEEITGPVDEETFLKAAVEGKMKVIEKFLADGGSADTCDQ--- 148
                                                                                                                                                                          127 TAFMEAAERGNAEALRFLFAKGANVNLRRQTTKDKRRLKQGGATALMSAAEKGHLEVLRI 186
                                                                                                                                                                                                                                                                                                                              68 SLDLRREII--DVGGIQNLIELRKKRKQKKRDALAASHEPPPEPEEITGPVDEEFFLKAA 125
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                                                                        41 VLEDEKHHGAQSAALQKVKGQERVRKTSLDLRREIIDVGGIQNLIE------LRKKRKQ 93
                                                                                                22 VVEDD-----SSLIKAVQKGDVVRV-----QQLLEKGADANACEDTWGWTPLHNAVQA 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: Mark D. Cochran and David E. Junker
TITLE OF INVENTION: Recombinant Fowlpox Viruses and Uses Thereof
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
                                      86;
Length 679;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 422;
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                                      Indels
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FILLING DATE: US/08/484,575A FILLING DATE: 07-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     98;
                                    41; Mismatches 101;
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; Pred. No. 4.6e-14;
48; Mismatches 98
Score 224; DB 5;
Pred. No. 7.3e-14;
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STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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NAME: White Esq, John P
TELECOMUNICATION INFORMATION:
TELEPHONE: (212)278-0450
TELEFAX: (212)391-0525
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
13.2%; 28.1%;
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Best Local Similarity 25.9%;
Matches 67; Conservative 48
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amino acid
                                      Conservative
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US-08*484-575A-6
  Query Match
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Matches 8
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223 AVRTGQVEIVEHFLSLGLEINARDREGDTALHDAVRLNRYKIIKLLLLHGADMMTKNLAG 282
                     68 SLDLRREII--DVGGIQNLIELRKKRRQKKRDALAASHEPPPEPEEITGPVDEETFLKAA 125
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                                                                                                                                                                               Sequence 6, Application US/08479869
Patent No. 6123949
GENERAL INFORMATION:
APPLICANT: Cochran Ph.D, Mark D
TITLE OF INVENTION: Recombinant Fowlpox Virus S-FPV-043 and
TITLE OF INVENTION: Uses Thereof
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSE: John P. White
STREET: 30 Rockefeller Plaza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 422;
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/08/479,869
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/024,156
FILING DATE: 26-FEB-1993
ATTORNEY/AGENT INFORMATION:
NAME: White Esq. John P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: White Esq. John P
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)977-9550
TELEFAX: (212)664-0525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: 6: SEQUENCE CHARACTERISTICS: THOUSEN 422 amin-
                                                                                       283 KTPTDLVQLWQADTRHALE 301
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amino acid
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Best Local Similarity 25.9%
Matches 67; Conservative
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MEDIUM TYPE: Floppy
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RY: USA
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CITY: New
STATE: Ne
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283 KTPTDLVQLWQADTRHALE 301
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Search completed: April 17, 2002, 08:10:35 Job time: 53 sec

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APPLICANT: Tang, Y. Tom
APPLICANT: Carley, Nail C.
APPLICANT: Vac, Henry
TITLE OF INVENTION: HUMAN ANKYRIN FAMILY PROTEIN
FILE REFERENCE: PF-0615 US
CURRENT APPLICATION NUMBER: US/09/172,977
CURRENT FILING DATE: 1998-10-14
NUMBER OF SEQ ID NOS: 4
SOFTWARE: PERL Program
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 233;
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Pred. No. 2.4e-10;
0; Mismatches 233;
               US-07-884-811-15
US-07-885-971-15
US-08-194-0888-15
US-08-194-0888-15
US-08-194-087-15
US-08-462-481-3
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US-08-471-5
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US-08-771-7
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Sequence 2, Application US/09172977; Patent No. 5989663
GENERAL INFORMATION:
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US-09-172-977-2
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Best Local Similarity 48.2
Matches 217; Conservative
3489
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    LENGTH: 1288
SEQ ID NO 2
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Compugen Ltd
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US-09-428-219-3

US-08-741-891-208

US-09-196-387-1

US-08-436-771-1

US-08-436-771-3

US-08-436-771-3

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US-08-436-771-3

US-08-447-998-3

US-08-487-797-3

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US-08-487-797-3

US-08-417-998-3

US-08-417-998-3

US-08-410-112-9

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                     GenCore version
Copyright (c) 1993 - 2000
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Maximum Match 100%
Listing first 45 summaries
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seq length: 2000000000
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                                                                                                                 APPLICANT: Dedhar, Shoukau
APPLICANT: Dedhar, Greg
APPLICANT: Hannigan, Greg
TITLE OF INVENTION: Integrin-Linked Kinase and
TITLE OF INVENTION: its Uses
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Pred. No. 4.5e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: FastSEQ for Windows Version 2.0
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Suite 200
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                                                                      Sequence 1, Application US/09035706
Patent No. 6001622
                                                                                                                                                                                                                                                                                         ADDRESSEE: Bozicevic & Reed,
STREET: 285 Hamilton Avenue,
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: K
FELECOMMUNICATION INFORMATION
TELEPHONE: 650-327-3400
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM Compatible OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: Sherwood, Pamela J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          UCENGTH: 1789 base pairs
LENGTH: 1789 base pairs
TYPE: nucleic acid
GTPANDEDNESS: double
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APPLICATION NUMBER: US
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: 650 327-3231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
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Best Local Similarity
                                                                                                                        GENERAL INFORMATION:
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TOPOLOGY: lin
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US-09-035-706-1
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                                             US-09-035-706-1
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APPLICANT: Morrow, Jon S.
APPLICANT: Devaration, Prasad
ATLE OF INVENTION: No. 6225086el Ankyrin Proteins and a Method for Their Identificat
FILE REFERENCE: 44574-5002-018
CURRENT APPLICATION NUMBER: 08/09/082,059A
CURRENT FILING DATE: 1998-05-21
EARLIER APPLICATION NUMBER: 60/047356
BARLIER FILING DATE: 1997-05-21
NUMBER OF SEQ ID NOS: 19
SOFTWARE: Patentin Ver. 2.0
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889 acgiggacaicaacaictaigaitggaaiggagggacgccacigcigiacgcigigcgcg 948
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; OTHER INFORMATION: DNA/protein segment- human kidney Ankyrin G119 (08-09-082-059-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1413 gctacatctcagtagtggacaccctgaagatagtgaccgaagaaaccatgacca 1466
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                                                                                                                                          Sequence 1, Application US/09082059A Patent No. 6225086 GENERAL INFORMATION:
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Best Local Similarity 47.5%;
Matches 225; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Homo sapiens
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LENGTH: 3454
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APPLICANT: C. Frank Bennett
APPLICANT: Lew M. COMSETT
TILLE OF INVENTION: ANTISENSE MODULATION OF INTEGRIN-LINKED KINASE EXPRESSION
FILE REFERENCE: RTS-0101
CURRENT APPLICATION NUMBER: US/09/428,219
CURRENT FILING DATE: 1999-10-27
NUMBER OF SEQ ID NOS: 89
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486 GGGCCAAGATCAAGTGGCAGAGGACCTGGTGGCAAATGGGGCCCTTGTCAGCATCTGTAA 545
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APPLICANT: Schellenberg, Gerald D.
TITLE OF INVENTION: GENE AND GENE PRODUCTS RELATED TO
TITLE OF INVENTION: WERNER'S SYNDROME
NUMBER OF SEQUENCES: 209
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Pred. No. 4.5e-07;
0; Mismatches 163;
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Patent No. 6090620
GENERAL INFORMATION:
APPLICANT: Fu, Ying-Hui
APPLICANT: Yu, Chang-En
APPLICANT: Oshima, Junko
                                                cctggcaggaaagaccccgacggac 880
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CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
                                                                                                                                                                                                      Sequence 3, Application US/09428219
Patent No. 6177273
GENERAL INFORMATION:
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Best Local Similarity 49.8%;
Matches 162; Conservative
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; LOCATION: (157)..(1515)
US-09-428-219-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5.5%; Score 64.2; DB 3; 49.8%; Pred. No. 4.5e-07;
                                                                                                                                                           Satent No. bullion:
GENERAL INFORMATION:
APPLICANT: Bondar, Shoukat
APPLICANT: Hannigan, Greg
TITLE OF INVENTION: Integrin-Linked Kinase and
TITLE OF INVENTION: its Uses
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEG for Windows Version 2.0
CURRENY APPLICATION DATA:
APPLICATION NUMBER: US/08/955,841
                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
CORRESSEE: Bozicovic & Reed, LLP
STREET: 285 Hamilton Avenue, Suite 200
Sequence 1, Application US/08955841
Patent No. 6013782
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Sherwood, Pamela J
REGISTRATION NUMBER: 36,677
REFERENCE/DOCKET NUMBER: KI
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-327-3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1789 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILLING DATE:
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Diskette
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TELEFAX: 650 327-3231
                                                                                                                                                                                                                                                                                                                                                                                                                                                         272: 24301
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                          USA
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2515 ATTCAACCCCTCTGCACCTGGCAGCTATAATAACCTGGAAGTAGCTGAATATCTTC 2574
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2755 AGCTGTGCGCCCTCCTCCTAGCGCATGGTGCAGACCCCACCATGAAGAACCAGGAAGGCC 2814
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2575 TAGAGCATGGAGCTGAŤGTTAATGCCCAGGACAAGGGTGGTTTAATTCCTCTTCATAATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           627 aaagccatggagcagacaccaatgtgagggataagctgctgagcaccccgctgcacgtgg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              747 atgccagagacagggaaggggatactgcctgcatgacgctgtgaggctcaaccgctaca
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APPLICANT: de Lange, Titia
APPLICANT: Smith, Suase
TITLE OF INVENTION: A PROTEIN THAT BINDS TO TRF1 AND METHODS
TITLE OF INVENTION: OF USE THEREOF
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 4134;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                     SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/196,387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 62; DB 4; Lei
Pred. No. 2.1e-06; O; Mismatches 160;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3: Klauber & Jackson
411 Hackensack Avenue, 4th Floor
                                                                                                                                                                                                                                                                                            600-1-230 CIP1
                                                                                                                    FILING DATE:
CLASSIFICATION
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/095,225
FILING DATE: June 10, 1998
ATTORNEY/ARGHT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
                 COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-196-387-7; Sequence 7, Application US/09196387; Patent No. 6277613
                                                                                                                                                                                                                                                                        REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 60
TELECOMMUNICATION INFORMATION:
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ilarity 49.7%;
Conservative (
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Floppy dis
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LENGTH: 4134 base pairs
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                        201-343-1684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: 411 HacketITY: Hackensack
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Best Local Similarity
Matches 158; Conservi
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: 11
MOLECULE TYPE:
MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; HYPOTHETICAL:
US-09-196-387-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               82 ggaggagaatgagaaactccgaggagacacacgccagaagctgcccatggacttgctggt 141
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   262 ccagaacctcatcgagctgcggaagaaacgcaagcagaagaagcggga 309
                                                                                                                                                          OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1, Application US/09196387; Patent No. 6277613; Patent No. 6277613; Application US/09196387; Patent No. 6277613; Applicant Information: Applicant: Smith, Susan TITLE OF INVENTION: A PROTEIN THAT BINDS TO TITLE OF INVENTION: A PROTEIN THAT BINDS TO TITLE OF INVENTION: A PROTEIN THAT BINDS TO TITLE OF INVENTION: A DIRECS: ADDRESS: ADDRESSER: All Hackensack Avenue, 4th Floor CITY: Hackensack STATE: New Jersey COUNTRY: USA
                                                                                                                                                                                                                                                                                          ATTORNEY AGENT INFORMATION:
NAME: NO. 6090620tenburg Ph.D., Carol
REGISTRATION NUMBER: 39,317
REFERENCE/DOCKET NUMBER: 34,317
RELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEPRA: (206) 682-6031
INFORMATION FOR SEQ ID NO: 208:
SEQUENCE CHARACTERISTICS:
LENGTH: 16442 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
                                                                                                                                                                                                                               APPLICATION NUMBER: US/08/781,891
FILING DATE: 27-DEC-1996
CLASSIFICATION: 800
                                                                                                                                               COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS
                                                                              ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 51.0
Matches 147; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       single
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                      Seattle
Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-781-891-208
                                                                   COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
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889 GCACATAGAGATTAATGACACAGAGAGAGAGAAAACAGCACTGCTGCTTGTTGA 948
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                                                                                                                  Smith, Schuster
                TITLE OF INVENTION: Animal 2-5A- Dependent RNases and TITLE OF INVENTION: Encoding Sequence Therefor
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/462,481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 61.8; DB 2;
Pred. No. 2.1e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
                           Patent No. 5840577
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Ruden, Barnett, McClosky,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Manso, Peter J
REGISTRATION NUMBER: 32,264
REFERENCE/DOCKET NUMBER: CL11363-13
TELECOMMUNICATION INFORMATION:
                                                                                                                                                     STREET: 200 East Broward Boulevard
CITY: Fort Lauderdale
STATE: Florida
                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/028,086
FILING DATE: 08-MAR-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                 PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1, Application US/08436771
Patent No. 5861300
GENERAL INFORMATION:
APPLICANT: Silverman, Robert H.
APPLICANT: SenGupta, Dibyendu N.
                                                                                                                                                                                                                                ZIP: 33301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 5.3%;
Best Local Similarity 57.8%;
Matches 130; Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: 305/764/4996
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 2928 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: 305/2-7
Zhou, Aimin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CDS
104..2326
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LOCATION:
                                                                                                                                                                                                                    COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-436-771-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2932 TAGAGCATGGAGCTGATGTTAATGCCCAGGACAAGGGTGGTTTAATTCCTCTTCATAATG 2991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cagtccggacagggcaggtggagattgtggagcactttctatccctgggcctggaaatca 746
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      567 actgcacagccatgcattgggcctgccgcgggggccacttagaggtggtgaaacttctgc 626
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Best Local Similarity 49.7%; Pred. No. 2.2e-06;
Matches 158; Conservative 0; Mismatches 160; Indels
                                                                                                                OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/196,387
                                                                                                                                                                                                                                                                                                                                                           600-1-230 CIP1
                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/095,225
FILLING DATE: June 10, 1998
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 9
US-08-462-481-1
Sequence 1, Application US/08462481
Sequence No. 5840577
GENERAL INFORMATION:
APPLICANT: APPLICANT: Hassel, Bret A.
                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                               NAME: Jackson Esg., David A. REGISTRATION NUMBER: 26,742
                                                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 201-343-1684
TELEX: 133521
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 4491 base pairs
                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy COMPUTER: IBM PC COMP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6..2027
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          linear
                                                                                                                                                                                                                    CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE:
                                                                                                                                                                                                 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; LOCATION:
US-09-196-387-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY:
                  COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                687
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WEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
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Pred. No. 2.1e-06;
0; Mismatches 92;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Manso, Peter J.
REGISTRATION NUMBER: 32,264
REFERENCE/DOCKET NUMBER: CL11363-16
TELECOMMUNICATION:
TELEPHONE: 305/527/2498
                                                                                                                                                                                                                                                                                                                                           CLASSIFCATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/198,973
FILING DATE: 18-FEB-1994
ATTORREY AGENT INFORMATION:
NAME: Manso, Peter J.
                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/436,771
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 5.3%;
Best Local Similarity 57.8%;
Matches 130; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS: LENGTH: 2928 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               305/764/4996
NUMBER OF SEQUENCES: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                  ZIP: 33301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CDS
104..2326
                                                                                                                                                                33301
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; LOCATION:
US-08-436-771-3
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US-08-434-998-1
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Patent No. 5861300
GENERAL INFORMATION:
APPLICANT: Silverman, Robert H.
APPLICANT: SenGupta, Dibyendu N.
APPLICANT: APPLICANT: APPLICANT: APPLICANT: TITLE OF INVENTION: Antiviral Transgenic Plants, Vectors, TITLE OF INVENTION: Cells and Methods
    TITLE OF INVENTION: Antiviral Transgenic Plants, Vectors, TITLE OF INVENTION: Cells and Methods
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          92; Indels
                                                                                    ADDRESSEE: Ruden, Barnett, McClosky, Smith, Schuster ADDRESSEE: Russell
STREET: 200 E. Broward Boulevard
STREET: Florida
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  793 geteaacegetacaaaateateaactgetgeteetgeatgggge 837
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                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5.3%; Score 61.8; DB 2;
illarity 57.8%; Pred. No. 2.1e-06;
Conservative 0; Mismatches 92;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Manso, Peter J.
KEJISTRATION NUMBER: 32,264
REFERENCE/DOCKET NUMBER: CL11363-16
TELECOMMUNICATION INFORMATION:
TELEPHONE: 305/764/4996
TELEFAX: 305/764/4996
                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/198,973
FILING DATE: 18-FEB-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/436,771
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CDS
104..2326
                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 536
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Best Local Similarity
Matches 130; Conserva
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                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
                                                                                                                                                                                                               ZIP: 33301
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; LOCATION:
US-08-436-771-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY:
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US-08-436-771-3
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889 GCACATAGAGATTAATGACACAGAGACAGTGATGGCAAAACAGCACTGCTGCTGTTGA 948
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Patent No. 5866781
GENERAL INFORMATION:
APPLICANT: Silverman, Robert H.
APPLICANT: Sendupta, Dibyendu N.
TITLE OF INVENTION: Cells and Methods
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Ruden, Barnett, McClosky, Smith, Schuster ADDRESSEE: Russell Barnett, McClosky, Smith, Schuster ADDRESSEE: Russell Broward Boulevard CITY: Fort Lauderdale STATE: Flortida COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          793 geteaacegetacaaaateateaaactgetgeteetgeatgggge 837
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33301
                     CITY: FO
STATE: F
COUNTRY:
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US-08-487-797-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       769 GCATCTGCTGCACCATGGGGCTGATGTCAATGTGAGGGGAAAAGAGGGAAAGACTCC 828
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           829 CCTGATCCTGGCAGTGGAGAAGCACTTGGGTTTGGTGCAGAGGCTTCTGGAGCAAGA 888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 61.8; DB 2; Length 2928;
Pred. No. 2.1e-06;
0; Mismatches 92; Indels 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-434-998-3
Sequence 3, Application US/08434998
TITLE OF INVENTION: Antiviral Transgenic Plants, Vectors, TITLE OF INVENTION: Cells and Methods
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ruden, Barnett, McClosky, Smith, Schuster & Russell
ADDRESSEE: Ruden, Barnett, McClosky, Smith, Schuster & ADDRESSEE: Russell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      793 getcaaccgetacaaaateateaaactgetgeteetgeatgggge 837
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPOTER: IBM PC Compatible
OPERATURG SYSTEM: PC-TOOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/198,973
FILING DATE: 18-FEB-1994
ATTORNEY/ACENT INFORMATION:
NAME: Manso, Peter J.
REGISTRATION NUMBER: 32,264
REGISTRATION NUMBER: CL11363-16
TELECOMMUNICATION:
TELEPHONE: 305/527/2498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CL11363-16
                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/434,998
                                     STREET: 200 E. Broward Boulevard
CITY: Fort Lauderdale
STATE: Florida
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 5.3%;
Best Local Similarity 57.8%;
Matches 130; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: 305/527/2498
TELEFAX: 305/764/4996
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2928 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               nucleic acid
EDNESS: single
                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; NAME/KEY: CDS
; LOCATION: 104..2326
US-08-434-998-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           linear
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                                                                                                                                                                                                                                                                                             FILING DATE:
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ADDRESSEE:
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616 gaaacttctgcaaagccatggagcagacaccaatgtgagggataagctgctgagcacccc 675
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Patent No. 5865787

GENERAL INFORMATION:

APPLICANT: Silverman, Robert H.

APPLICANT: SenGupta, Dibyendu N.

TITLE OF INVENTION: Transgenic Plants Co-Expressing A

TITLE OF INVENTION: Functional Human 2-5A System

NUMBER OF SEQUENCES: 11

CORRESPONDENCE ADDRESS:

ADDRESSEE: Holland & Knight

STREET: One E. Broward Boulevard, #1300

CITY: Fort Lauderdale

STATE: Florida
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    793 gctcaaccgctacaaaatcatcaaactgctgctcctgcatggggc 837
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APPLICATION NUMBER: US/08/434,998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 5.3%; Score 61.8; DB 2; Best Local Similarity 57.8%; Pred. No. 2.1e-06; Matches 130; Conservative 0; Mismatches 92;
                                                                                                                                                                                                                                                                                     FILING DATE:
CLASSIFICATION: 800
PRICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 08/198,973
FILING DATE: 18-FEB-1994
ATTORNEY/AGENT INFORMATION:
NAME: MANSO, PELER J.
REGISTRATION NUMBER: 32,264
REFERENCE/DOCKET NUMBER: CL11363-16
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION SOS 32,527/2498
TELEFAX: 305/764/4996
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
: 200 E. Broward Boulevard
Fort Lauderdale
Florida
                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
CMDTUPTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 2928 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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; LOCATION: 104..2326
US-08-434-998-3
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Search completed: April 17, 2002, 09:28:45 Job time: 4769 sec
SOFTWARE: Patentin Rel
CURRENT APPLICATION DATA
APPLICATION NUMBER: US
                                                                                                                                                                                                                                                                                                            linear
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EOCATION:
US-08-487-797-3
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APPLICANT: SenGupta, Dibyendu N.
TITLE OF INVENTION: Transgenic Plants Co-Expressing A
TITLE OF INVENTION: Functional Human 2-5A System
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Holland & Knight
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       793 geteaacegetacaaaateateaaactgetgeteetgeatgggge 837
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,797
FILING DATE: 07-JUNE-1995
CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 61.8; DB 2;
Pred. No. 2.1e-06;
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STREET: One B. Broward Boulevard, #1300
CITY: Fort Lauderdale
STATE: Florida
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 5.3%; Score 61.8; Dest Local Similarity 57.8%; Pred. No. 2.1e Matches 130; Conservative 0; Mismatches
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COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: Manso, Peter J.
REGISTRATION NUMBER: 32,264
REFERENCE/DOCKET NUMBER: CL11
TELECOMMUNICATION INFORMATION:
TELEPHONE: 305/468-7811
TELEFEAX: 305/463-2030
                                                                                                                                                                                                                                                                                                                                                LENGTH: 2928 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
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ZIP: 33301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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; LOCATION: 104..2326
US-08-487-797-1
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Patentin Release #1.0, Version #1.25
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Pred. No. 2.1e-06;
0; Mismatches 92;
                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: Wanso, Peter J.
REGISTRATION NUMBER: 32,264
REBRENCE/DOCKET NUMBER: CL11363-16(C)
TELECOMMUNICATION INFORMATION:
TELEPHONE: 305/468-7811
TELEPRAX: 305/463-7310
INFORMATION FOR SEQ ID NO: 35EQUENCE CHARACTERISTICS:
LENGTH: 2928 base pairs
                                                                                                                                                                                                                                                                                                                                                     DNA (genomic)
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                                                    FILING DATE: 07-JUNE-1995
CLASSIFICATION: 800
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Matches 130; Conservative
                                                                                                                                                                                                                                                                                            TYPE: nucleic acid
STRANDEDNESS: single
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104..2326
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Thu Apr 18 10:26:06 2002

GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.

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                              April 17, 2002, 08:09:16; Search time 175.48 Seconds
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Maximum Match 100%
Listing first 45 summaries
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AAI60004
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## ALIGNMENTS

Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer; peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; hauthington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation; Human polynucleotide SEQ ID NO 1712. BP. AAI59509 standard; cDNA; 1208 2000US-0488725. 2000US-0552317. 2000US-0598042. 2000US-0620312. 2000WO-US34263 2000US-0653450 2000US-0662191 2000US-0693036 2000US-0727344 (first entry) WO200153312-A1. leukaemia; ss 14-SEP-2000; 19-OCT-2000; 29-NOV-2000; Homo sapiens. 26-DEC-2000; 21-JAN-2000; 25-APR-2000; 09-JUL-2000; 19-JUL-2000; 03-AUG-2000; 22-OCT-2001 26-JUL-2001 AAI59509; AA159509 RESULT THOM SEE A STANDARD S ~

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                                                                                                                                                                                                                                                           The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAM36642-AAM42213) with noctropic, finanuosouppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral nervopathy and localised neuropathies and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression, Activinibin activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, cancer diagnosis and therapy, drug screening,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       assays for receptor activity, arthritis and inflammation, leukaemias and C.N.S disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Note: The sequence data for this patent did not form part of the printed specification.
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                                      Wang
                                                                                                                                                                     Novel nucleic acids and polypeptides, useful for treating disorders such as central nervous system injuries -
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Pred. No. 1.1e-267;
                                  Ren F, W
Zhang J;
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                                    Qian XB,
Yang Y,
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                                  en R, Ma Y, (
u C, Xue AJ,
Drmanac RT;
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                                                                                                                                                                                                                             Claim 1; SEQ ID NO 1712; 10078pp; English.
                            Liu C, Asundi V, Chen R, Wang Z, Wehrman T, Xu C, Zhou P, Goodrich R, Drman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 99.9%;
Matches 1149; Conservative
                                                                                                            WPI; 2001-442253/47.
(HYSE-) HYSEQ INC
                                                                                                                                P-PSUB; AAM40353
                                                          Wang J,
Zhao QA,
                                  Tang YT,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
                                                                                                                   gcaccccgctgcacgtggcagtccggacagggcaggtggagattgtggagcactttctat
                                                                                                                                         actgagggcccagcctttttctgcatgatccaggagcacataccacaaactaccacat
                                                       cagetacceageceetetetgtgtgeageeggagggteetaagaatggeteeeggageta
                                                                                          gcaccccgctgcacgtggcagtccggacagggcaggtggagattgtgtggagcactttctat
                                                                                                                                                                                                    acttccaggatcggctggactgcacagccatgcattgggcctgccgcggggggccacttag
                                            aggtggtgaaacttctgcaaagccatggagcagacaccaatgtgagggataagctgctga
                                                                                                                                                                                         tgaggetcaaccgetacaaatcatcaaactgetgetectgeatggggetgacatgatga
                     acttccaggatcggctggactgcacagccatgcattgggcctgccgcgggggccacttag
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25-APR-2000; 2000US-0552317.
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                                                                                                                                                                                                                                                                                                                                                                                                                                The sequence data for this patent did not form part of the printed
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                                                                                                                 Wang
                                                                                                                                                                                                Novel nucleic acids and polypeptides, useful for treating disorders \text{such} as central nervous system injuries -
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Zhang J
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Yang Y,
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Pred. No. 2.3e-122;
                                                                                                             Chen R, Ma Y,
Xu C, Xue AJ,
R, Drmanac RT;
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                                                                                                                                                                                                                                 Claim 1; SEQ ID NO 5284; 10078pp; English.
                                                                                                             Asundi V, Che
Wehrman T, Xu
Goodrich R,
; 2000US-0598042.
; 2000US-0620312.
; 2000US-0653450.
; 2000US-0653191.
; 2000US-0693036.
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Matches 546; Conservative
                                                                                                                                                            2001-442253/47
                                                                                                             Liu C, F
Wang Z, V
Zhou P,
                                                                                      (HYSE-) HYSEQ INC.
                                                                                                                                                                         P-PSDB; AAM42139
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                                    14-SEP-2000;
19-OCT-2000;
29-NOV-2000;
                         03-AUG-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention provides the protein and coding sequences of number of human shear stress response proteins. These are useful ir diagnosis, treatment and screening of vascular diseases caused by
  gctgacgggggggtcagccgacacgtgcgaccagttccgtcggacagcactgcaccgagct
                            ccagagcccgaggagatcactggccctgtggatgaggagaccttcctgaaagctgcggtg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          encoded by them and antibodies against treatment of vascular disease caused by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 22; Length 1901;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; shear stress-response protein; vascular disease; arteriosclerosis; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human shear stress-response coding sequence SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1901 BP; 592 A; 378 C; 460 G; 471 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ouery Match 21.5%; Score 248.4; DB 22; Best Local Similarity 64.7%; Pred. No. 1.4e-50; Matches 369; Conservative 0; Mismatches 201;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ota T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             H, Obayashi M, Ota T, Nakamura Y, Sugano S;
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                                                                                                                                                                                                                                                                                                                                                                                                             AAH02910 standard; DNA; 1901 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (KYOW ) KYOWA HAKKO KOGYO KK. (NOJI/) NOJIMA H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99JP-0280976.
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Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;
gene therapy; chromosome mapping; ss.
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                                                                                                                                                                                                                                                                                   gagaagttaatggaagctggagcccagatcgaattccgtgatatgcttgaatccacagcc 816
                                                                                                  637
                                                                                                                              876
                                                                                                                                                      gcagacaccaatgtgagggataagctgctgagcacccgctgcacgtggcagtccggaca 697
                                                                                                                                                                        966
                                          577
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                                                                                                                                                                                                              gggcaggtggagattgtggagcactttctatccctgggcctggaaatcaatgccagagac 757
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New nucleic acid that is a 5' expressed sequence tag (5' EST) for obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for diagnostic, forensic, gene therapy and chromosome mapping procedures
                                                                                                                        817 atccactgggcaagccgtggaggaaacctggatgttttaaaattgttgctgaataaagga
                                                                                              578 atgcattgggcctgccgcgggggccacttagaggtggtgaaacttctgcaaagccatgga
                                                                                                                                                                                                                                       937 ggccactatgagtgcgcggagcatcttatcgcctgtgaggcagacctcaacgccaaagac
                                                                                                                                                                                                                                                                    agggaaggggatactgcctgcatgacgctgtgaggctcaaccgctacaaaatcatcaaa
                                                                                                                                                                                                                                                                                                                        818 ctgctgctcctgcatggggctgacatgatgaccaagaacctggcaggaaagaccccgacg
                                         gagaagettetagataatggggceactgtggaettecaggateggetggaetgeacagee
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human secreted protein 5' EST, SEQ ID NO: 20238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Giordano J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; SEQ ID 20238; 71pp + CD-ROM; English.
                                                                                                                                                                                                                                                                                                                                                                               Duclert A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAC16163 standard; cDNA; 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21-FEB-2000; 2000EP-0200610
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5' EST;
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           697
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libraries. Such ESTs are not well suited for isolating cDNA sequences derived from the 5' ends of mRNAs and even in those cases where longer cDNA sequences have been obtained, the full 5' UTR is rarely included. 5' ESTs are derived from mRNAs with intext 5' ends and can therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used in diagnostic, forensic, gene therapy and chromosome mapping procedures. They are used to obtain upstream regulatory sequences and to design
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                D, Klinger J, Kassam A;
Lamson G, Drmanac R;
Leshkowitiz D;
                                                                                                                                                                                                                                                      186
                                                                                                                                                                                                                                                                                                                               131 catggacttgctggtgctggaggatgagaagcaccacggggctcagagtgcagcctgca 190
                                                                                                                                                                                Gaps
                                                                                                                                                                                                        67
                                                                                                                                                                                                                                70
                                                                                                                                                                                                     8 agggacggcaccatggaggactccgaggcggtgcagaggccacagcgctcatcgagcag
                                                                                                                                                                                                                       catggacttgctggtgctggaggatgagaagcaccacggggctcagagtgcagccctgca
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or
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cytostatic; gene therapy; colon cancer; prostate cancer; cancer; lung cancer; cancer detection; ss.
                                                                                                                                                       Length 221;
                                                                                                                                                                               Indels
                                                                                                                                     Score 192.8; DB ZI,
                                                                                                                Sequence 221 BP; 54 A; 54 C; 87 G; 24 T; 2 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Garcia PD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Innis MA, Garcia PD,
Kennedy GC, Pot D, L
Dickson M, Labat I,
LW, Strache-Crain B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ID NO: 1819
                                                                                                                                                                               0; Mismatches
                                                                                                                                                                                                                                                                                                                                                        gaaggtgaagggccaagagcgcgtgcgc 214
                                                                                                                                                                                                                                                                                                                                                                      Claim 9; Page 804; 1046pp; English
                                                                                         expression and secretion vectors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                               ВР
                                                                                                                                                      16.6%;
98.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                            AAF66063 standard; cDNA; 386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99US-0142310.
99US-0142311.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel human polynucleotide,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30-JUN-2000; 2000WO-US18374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Williams LT, Escobedo J, Reinhard C, Randazzo F,
                                                                                                                                                   Query Match
Best Local Similarity 98.6
Matches 205; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Jones
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (CHIR ) CHIRON CORP. (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2001-091805/10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Garcia V,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO200102568-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      02-JUL-1999;
02-JUL-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human;
breast
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The present sequence is one of 3351 sequences in a library of human polynucleotides. The library is used to detect differentially expressed genes correlated with a cancerous state of a mammalian cell and can detect colon, prostate, breast and lung cancer. The library can be used to produce probes for detection of mRNA and to produce additional copies of the polynucleotides. The probes can be used for chromosome mapping of the polynucleotide and for detection of transcription levels. Ribozymes or antisense oligonucleotides can be generated. The polynucleotides and their gene products are used as genetic or biochemical markers (e.g. in blood or tissues) that will detect the earliest changes along the carcinogenesis pathway and/or monitor the efficacy of therapies and preventive interventions. The polynucleotides, polypetides and antibodies against them can be used in pharmaceutical compositions to the cancers and proliferative disorders such as neoplasia,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Garcia PD, Klinger J, Kassam A;
Pot D, Lamson G, Drmanac R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      351
                                                                                                                                                                                                                                                                                                                                                                                       338 ccagagcccgaggagatcactggccctgtggatgaggagaccttcctgaaagctgcggtg 397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                      112 ccagaacctgaaatcattacggaacctgtggatgtgcctacgtttctgaaggctgctctg 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                        gagggaaaatgaaggtcattgagaagttcctggctgacgggggggtcagccgacacgtgc 457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gaccagttccgtcggacagcactgcaccgagcttccctggaaggccacatggaaatcctg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gagaagettetagataatggggeeaetgtggaetteeaggateggetggaetgeaeagee
                                                                                                                                                                                                                                                                                                                                                       ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cytostatic; gene therapy; colon cancer; prostate cancer; cancer; lung cancer; cancer detection; ss.
                                                                                                                                                                                                                                                                                                                       DB 22; Length 386;
                                                                                                                                                                                                                                                                                                                     Score 113.4; DB 22; Length
Pred. No. 3.1e-18;
0; Mismatches 101; Indels
                                                                                                                                                                                                                                                                     Sequence 386 BP; 135 A; 68 C; 97 G; 86 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        atgcattgggcctgccgcgggggccacttagaggt 612
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel human polynucleotide, SEQ ID NO: 1804
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Escobedo J, Innis MA,
Randazzo F, Kennedy GC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAF66048 standard; cDNA; 363
                                                                                                                                                                                                                                                                                                                     9.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99US-0142310.
99US-0142311.
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                                                                                                                                                                                                                                     dysplasia and hyperplasia.
                                                                                                                                                                                                                                                                                                                                                    Matches 174; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (CHIR ) CHIRON CORP. (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                      Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200102568-A2.
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Reinhard C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
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                                                                                                                                                                                                                                                                                                                        Query Match
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breast
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The present sequence is one of 3351 sequences in a library of human polynucleotides. The library is used to detect differentially expressed genes correlated with a cancerous state of a mammalian cell and can detect colon, prostate, breast and lung cancer. The library can be used to produce probes for detection of mRNA and to produce additional copies to produce probes for detection of mRNA and to produce additional copies or antisense oligonucleotides. The probes can be used for chromosome mapping of the polynucleotide and for detection of transcription levels. Ribozymes or antisense oligonucleotides can be generated. The polynucleotides and their gene products are used as genetic or biochemical markers (e.g. in blood or tissues) that will detect the earliest changes along the carcinogenesis pathway and/or monitor the efficacy of therapies and preventive interventions. The polynucleotides, polypeptides and preventive interventions. The polynucleotides, polypeptides and create the cancers and proliferative disorders such as neoplasia, dysplasia and hyperplasia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer; per.pheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        338 ccagagcccgaggagatcactggccctgtggatgaggagaccttcctgaaagctgcggtg 397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gaggggaaaatgaaggtcattgagaagttcctggctgacgggggggtcagccgacacgtgc 457
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      172 gagaataaactgccagtagtagaaaaattcttgtcagacaagaacaatccagatgtttgt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            458 gaccagitccgicggacagcactgcaccgagcitccciggaaggccacaiggaaatccig
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or
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                                                                                          Library of polynucleotides for diagnosing a cancerous state of mammalian cell and detecting cancer, particularly of the colon prostate, comprises 3351 human polynucleotide sequences -
  Leshkowitiz D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 363;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 103.8; DB 22;
Pred. No. 6.3e-16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 363 BP; 128 A; 63 C; 87 G; 85 T; 0 other;
Drmanac S, Dickson M, Labat I, V, Jones LW, Strache-Crain B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human polynucleotide SEQ ID NO 3993.
                                                                                                                                                                      Claim 9; Page 802; 1046pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAI60004 standard; cDNA; 1783
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 9.0°
Best Local Similarity 63.3°
Matches 159; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      578 atgcattgggc 588
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                                                      WPI; 2001-091805/10.
                  Garcia V,
  Crkenjakov R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               leukaemia; ss
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                    Kita D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    398
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 and thrombolytic activity, cancer diagnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The sequence data for this patent did not form part of the printed
                                                                                                                                                                                                                                                                                     Wang D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   461
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      342 gtcaatttactcttggccaaaggggcaaatatcaatgcatttgacaagaaggaccggcgt 401
                                                                                                                                                                                                                                                                                                                                                                                              Novel nucleic acids and polypeptides, useful for treating disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      515 ctggagaagcttctagataatggggccactgtggacttccaggatcggctggactgcaca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gocatgcattgggcctgccgcgggggccacttagaggtggtgaaacttctgcaaagccat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   402 gctctgcactgggcagcatacatgggccacttggatgttgtagcattgctcattaaccat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ggagcagacaccaatgtgagggataagctgctgagcaccccgctgcacgtggcagtccgg
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                                                                                                                                                                                                                                                                                   Ren F, W
Zhang J;
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                                                                                                                                                                                                                                                                                     Qian XB,
Yang Y,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 96.8; DB 22;
Pred. No. 4.9e-14;
0; Mismatches 147;
                                                                                                                                                                                                                                                                                 Chen R, Ma Y, Q
Xu C, Xue AJ,
;, Drmanac RT;
                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; SEQ ID NO 3993; 10078pp; English
                                                                                                                                                                                                                                                                                                                                                                                                               such as central nervous system injuries
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                                                                                                                                                                                                                                                                                 Liu C, Asundi V, Ch
Wang Z, Wehrman T, X
Zhou P, Goodrich R,
                                                                                                                                                                      2000US-0653450.
2000US-0662191.
2000US-0693036.
                                                                                                         2000US-0488725.
2000US-0552317.
2000US-0598042.
2000US-0620312.
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                                                                             2000WO-US34263
                                                                                                                                                                                                                      2000US-0727344
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Best Local Similarity 55.7
Matches 185; Conservative
                                                                                                                                                                                                                                                                                                                                                2001-442253/47
                                                                                                                                                                                                                                                     (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                               P-PSDB; AAM40848
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              WO200153312-A1.
                                                                           26-DEC-2000;
                                                                                                                                                                        03-AUG-2000;
14-SEP-2000;
                                                                                                                           25-APR-2000;
09-JUL-2000;
                                                                                                                                                           19-JUL-2000;
                                                                                                                                                                                                     19-OCT-2000;
29-NOV-2000;
                                                                                                           21-JAN-2000;
                                            26-JUL-2001
                                                                                                                                                                                                                                                                                                                  QA,
                                                                                                                                                                                                                                                                                     rang YT,
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The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAM36642-AAM42213) with nootropic, the encoded polypeptides (AAM36642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polymucleotides are useful in gene therapy. A composition containing a polypeptide or polymucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous system diseases, such as lateliner's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclearosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression. Activin/inhibin activity, chemotexic/chemokinetic activity, haemostatic and thrombolytic activity, cancer diagnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and consistent of the printed consistent of the printed
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                                                                                                                                                                                                                          Human; nootropic; immunosuppressant; cytostatic; gene therapy; cances peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's, Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-brager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Wang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                useful for treating disorders
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Zhang J;
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Yang Y,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel nucleic acids and polypeptides, us such as central nervous system injuries
                 755 gacagggaaggggatactgcctgcatgacgc
                                                                                                                                                                                              Human polynucleotide SEQ ID NO 421
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Wang Z, Wehrman T, Xi
Zhou P, Goodrich R,
                                                                                                      AAI58218 standard; cDNA; 2894
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2000US-0552317.
2000US-0598042.
2000US-0620312.
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2000US-0662191.
2000US-0693036.
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                                                                                                                                                                 (first entry)
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P-PSDB; AAM39062.
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09-JUL-2000;
19-JUL-2000;
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19-OCT-2000;
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Wang J, W
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808 A; 627 C; 741 G; 718 T; 0 other;

Sequence 2894 BP;

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AAC76497;
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAH57161 to AAH57576 represent cell and tissue specific polynucleotide sequences (I). (I) can have cytostatic, immunomodulatory and neuroprotective activities, and can be used in gene therapy. (I) and proteins (II) encoded by then are used in high throughput screening assays to select DNA molecules, RNA molecules, peptide nucleic acids, mimetics, peptides, proteins, agonists, antagonists, antibodies or
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                                                                                                                   315 tecgaecgagggggggggeacageettgeaceatgeggetetgaaeggeeacgtggagatg 374
                                                                                                                                                                                         375 gtcaatttactcttggccaaaggggcaaatatcaatgcatttgacaagaaggaccggcgt 434
                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New cell and tissue specific polynucleotides useful for diagnosis, prognosis or monitoring of treatments for disorders where the gene associated with a cancer, immunopathology or neuropathology -
                                                                                                                                                                                                                                                                                                                    || ||||||||| | | | |||||||| | ggcgcagaagttatacccctctgcatgctgcagcctcc
                                                                                                                                                                                                                            gccatgcattgggcctgccgcgggggccacttagaggtggtgaaacttctgcaaagccat
                                                                                    tgcgaccagttccgtcggacagcactgcaccgagcttccctggaaggccacatggaaatc
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                                                                                                                                                                                                                                                                                                                                                                   acagggcaggtggagattgtggagcactttctatcctgggcctggaaatcaatgccaga
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human skeletal muscle cell specific cDNA sequence SEQ ID NO:220.
                                                 ;
0
                  2894;
                Length
                                                 Indels
              Score 96.8; DB 22;
Pred. No. 5.7e-14;
0; Mismatches 147;
                                                                                                                                                                                                                                                                                                                                                                                                                                       gacagggaagggatactgcctgcatgacgc 786
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        615 aatgtctatggaaatacagcgcttcacatcgc 646
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ВР
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              8.4%;
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                                 Similarity
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Human; open reading frame; ORFX; detection; cytostatic; hepatotropic; vulnerary; antipsoriatic; antiparkinsonian; nootropic; neuroprotective; anticonvulsant; osteopathic; antiarthritic; immunosuppressant; cardiant;
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their fragments, immunoglobulins, inhibitors, drug compounds and pharmaceutical agents. Expression of (1) in a sample indicates the differentiation of embryonic stem cells into a tissue selected from brain, heart, kidney, liver, lung, skeletal muscle or pancreatic tissues. (1) and (11) are used to produce an expression profile that defines a metabolic or developmental process, treatment, condition, disease or disorder. The gene profile can be used for diagnosis, prognosis or monitoring of treatments and for investigating a predisposition to a disorder where the gene is associated with a cancer, immunopathology or neuropathology.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  immunostimulant; thrombolytic; coagulant; vasotropic; antidiabetic;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 7185 BP; 1735 A; 2049 C; 2047 G; 1326 T; 28 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7.5%; Score 86.6; DB 22;
llarity 47.9%; Pred. No. 2.1e-11;
Conservative 0; Mismatches 304;
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Matches 282; Conserv
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1448 aaggccactacgaagtggtccagtacctgctttcaaatggacggatggacgtcaactgtc 1507

aaggccacatggaaatcctggagaagcttctagataatg---gggccactgtggacttcc

498

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1508 aggatgacggaggctggacacccatgatctgggccacagagtacaagcacgtggacctcg 1567

aggatcggctggactgcacagccattggactgcctgccggggggccacttagaggtgg

1568 tgaagctgctgctgtccaagggctctgacatcaacatccgagacaacgaggagaacattt 1627

tgaaacttctgcaaagccatggagcagacaccaatgtgagggataagctgctgagcaccc

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675

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735

cgctgcacgtggcagtccggacagggcaggtggagattgtggagcactttctatccctgg gcctggaaatcaatgccagagacagggaaggggatactgccctgcatgacgctgtgaggc 1688 agtgcgacetccacgccgtgaacatccacggagactcgccactgcacattgccgcccggg 795 tcaaccgctacaaaatcatcaaaactgctgctcctgcatggggctgacatgatgaccaaga

734

1748 agaaccgctacgactgtgtcgtcctctttcttctgggattcagatgtcaccttaaaga 1807

g ă AAH46914 standard; cDNA; 2348

AAH46914

(first entry)

25-SEP-2001

AAH46914;

855 acctggcaggaaagacccc 873

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AAC74446 to AAC77606 encode the proteins given in AAB40237 to AAB43397, which represent the human ORFX open reading frames 1 to 3161. The ORFX sequences have activities such as: cytostatic; hepatotropic; vulnerary; antiparkinsonian; nootropic; neuroprotective; osteopathic; anticonvulsant; antiarthritic; immunosuppressant; immunostimulant; cardiant; thrombolytic; coagulant; vasotropic; antidiabetic; hypotensive; dermatological; immunosuppressive; antidiflammatory; antibacterial; antiviral; antifungal; antirheumatic; antithiflammatory antibacterial; antiviral; antifungal; antirheumatic; antithyroid; and antianeamic. The sequences can be used for determining the presence of or predisposition to, or preventing or treating pathological conditions associated with an ORFX associated disorder. The
                                           hypertension;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        nucleic acids can be used to express ORFX proteins in gene therapy vectors. The proteins and nucleic acids may be used to treat cancers, proliferative disorders, neurodegenerative disorders, osteoarthritis, graft vs host disease, cardiovascular disease, diabetes mellitus, hypertension, hypothyroidism, cholesterol ester storage, systemic lupus
                                                                                                     cholesterol ester storage; systemic lupus erythematosus; infection; severe combined immunodeficiency; malaria; autoimmune disorder; asthma; allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound; bone damage; cartilage damage; antiinflammatory disease; coagulation; thrombosis; contraceptive; a
                                    antianaemic; gene therapy; cancer; proliferative disorder; hypertension
neurodegenerative disorder; osteoarthritis; graft vs host disease;
cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel nucleic acids and peptides derived from open reading frame X,
dermatological; immunosuppressive; antiinflammatory;
                  antibacterial; antifungal; antirheumatic; antithyroid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            useful for treating e.g. cancers, proliferative disorders, neurodegenerative disorders and cardiovascular disease -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 5; Page 3287-3289; 5507pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                 31 MAR-1999; 99US-0127607.
02-APR-1999; 99US-0127636.
05-APR-1999; 99US-0127728.
30-MAR-2000; 2000US-0540763.
                                                                                                                                                                                                                                                                                                                                                                          31-MAR-2000; 2000WO-US08621
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Leach M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (CURA-) CURAGEN CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2000-602362/57.
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antiparkinsonian, virucidė, antibacterial, antifungal, antimigraine, analgesic, hypotensive, hypertensive, immunosuppressive, antiallergic, antipsoriatic, antirheumatic, antiarthritic, ophthalmological, anorectic, osteopathic, thrombolytic, antiarteriosclerotic, antiasthmatic,
                                                           Protein kinase; enzyme; cytostatic; nootropic; neuroprotective; human;
                                                                                                                                                                                                                                                                                                                                                                  Martinez R;
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                                                                                                                                                                                                                                                                                                                                                                  Sudarsanam
                                                                                                                vasotropic; antidiabetic; gene therapy; ss.
                                        cDNA encoding human protein kinase SGK288.
                                                                                                                                                       Location/Qualifiers
54..2348
/*tag= a
                                                                                                                                                                                                                                                                                                                                                                  Manning G,
                                                                                                                                                                                                                                              2001WO-US02337
                                                                                                                                                                                                                                                                                       2000US-0183173
2000US-0190162
                                                                                                                                                                                                                                                                                                                       2000US-0247013
                                                                                                                                                                                                                                                                                                              2000US-0193404
                                                                                                                                                                                                                                                                                                                                                                  Whyte D,
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                                                                                                                                                                                                                                                                                                                                             (SUGE-) SUGEN INC
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                                                                                                                                                                                                    WO200155356-A2
                                                                                                                                                                                                                                                                                                  17-MAR-2000;
29-MAR-2000;
13-NOV-2000;
                                                                                                                                                                                                                                              25-JAN-2001;
                                                                                                                                      sapiens
                                                                                                                                                                                                                                                                    25-JAN-2000;
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erythematosus, severe combined immunodeficiency (SCID), AIDS, viral, bacterial or fungal infection, malaria, autoimmune disorders, asthma, allergies, aplastic anaemia, burns, wounds, bone and cartilage damage,

haemoglobinuria, antiinflammatory disease; to enhance

coagulation; to inhibit thrombosis; and as a contraceptive.

Sequence 3040 BP; 680 A; 915 C; 934 G; 506 T; 5 other;

1328 cgttgatggaagcagccgaaaacaaccatctggaagcagtgaagtacctcatcaaggctg 1387

ccttcctgaaagctgcggtggagggaaaatgaaggtcattgagaagttcctggctgacg

Length 3040;

DB 21;

7.3%; Score 84.6; DB 21; 49.5%; Pred. No. 5e-11; tive 0; Mismatches 249;

al Similarity 49.5 247; Conservative

Query Match Best Local Si Matches 247,

378

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438

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1388 gggccctggtggatcccaaggacgcagaggctctacgtgtttgcacctggctgccaaga 1447

gggggtcagccgacacgtgcgaccagttccgtcggacagcactgcaccgagcttccctgg 497

RESULT

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cargines and polynucleotides encoding the polypeptides. The kinase polypeptides and their modulators are useful for treating a disease or disorder such as cancer, immune-related diseases, cardiovascular disease, brain or neuronal-associated disease and metabolic disorders, including cancers of tissues, cancers of hematopoietic origin, diseases of the central nervous system, diseases of the peripheral nervous system.

Alzheimer's disease, Parkinson's disease, multiple sclerosis, amyotrophic lateral sclerosis, viral infections, infections caused by prions, mood disorders, attention disorders, pain, sexual dysfunction, mood disorders, attention disorders, neurological disorders, dyskinesias, hypertension, psychotic disorders, neurological disorders, dyskinesias, for treating rhinitis, autoimmunity, atherosclerosis, psoriasis, costecarthritis, asthma, chronic inflammatory pelvic disease, chronic inflammatory bowel disease, rheumatoid arthritis, metabolic disorders and atherosclerosis, such as diabetes, obesity, cardiovascular diseases such as reperfusion, injury, coronary thrombosis, clothing disorders and atherosclerosis, coular diseases such as diseases such as diseases such as diseases such as diseases are described as diseases and a delegant relation, collegant relations and advantance diseases are described as diseases and a diseases and a delegant relation, collegant diseases are as glaucoma, retinopathy and macular desentation,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       dementia, manic depression, etc. The polynucleotides are useful in gene therapy techniques to treat the above mentioned disorders. Sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAH46891-46922 represent human protein kinases encoding cDNA molecules.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          neurological disorders such as anxiety, schizophrenia,
Kinase polypeptides useful for treating cancers, Alzheimer's disease, viral infections, diabetes, obesity, organ transplant rejection and
                                                                                                                                                                                                         invention provides human protein kinases and protein kinase-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 2348 BP; 516 A; 717 C; 696 G; 419 T; 0 other;
                                                                                                                                         Example 1; Page 210; 218pp; English.
                                      viral infections, dial
rheumatoid arthritis
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                                                                                            389 gctgcggtggaggggaaaatgaaggtcattgagaagttcctggctgacgggggggtcagcc 448
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0
Length 2348;
                                               Indels
Score 79.2; DB 22;
Pred. No. 9.3e-10;
); Mismatches 268;
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  6.8%;
                                               Conservative
                         Similarity
                         Best Local Sim
Matches 240;
       Query Match
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589 acgaggigicagototigocggocaccotagactocotgicoatocaccagotogoageac 648

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2232 acaccctgcaactggccctccgcagcc 2259 accccgacggacctggtgcagctctggc 896

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This sequence encodes the human ankyrin family protein, ANFP, of the invention. Host cells containing an expression vector containing the polynucleotide sequence can be cultured to produce ANFP, which can be used for diagnosis or treatment of autoimmune, inflammatory, proliferative and vesicle-trafficking disorders. Disorders which can be proliferative and vesicle-trafficking disorders. Disorders which can be treated include acquired immune deficiency syndrome (AIDS), allergies, amyloidosis, anaemia, asthma, atherosclerosis, bronchitis, Crohn's disease, atopic dermatitis, diabetes mellitus, irritable bowel syndrome, myocardial or pericardial inflammation, osteoporosis, rheumatoid contraction probe to detect ANFP-encoding polynucleotides and so be used as a hybridisation probe to detect ANFP-encoding polynucleotides in biological camples. Purified ANFP can be used to produce antibodies or to screen libraries of pharmaceutical agents to find agents that specifically bind ANFP. The DNA and its antisense sequence can be used in therapeutic compositions en of the compositions en of the absence and excess of confidence and to indicate the absence and excess of contraction in solution of ANFP and monitor its levels during therapeutic
                                                                                                                                                                        Human; ankyrin family protein; ANFP; autoimmune disorder; inflammation; atherosclerosis; inflammatory disorder; proliferative disorder; AIDS; secletrafficking disorder; allergy; amyloidosis; anaemia; asthma; bronchitis; crohn's disease; atopic dermatitis; diabetes mellitus; irritable bowel syndrome; osteoporosis; rheumatoid arthritis; cirrhosis; hepatitis; ulcerative colitis; cancer; hypercholesterolaemia; therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Polynucleotide sequence encoding a human ankyrin family protein useful for diagnosis or treatment of autoimmune, inflammatory, proliferative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           435 acgggggggtcagccgacacgtgcgaccagttccgtcggacagcactgcaccgagcttccc 494
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                                                                                                                                       Human ankyrin family protein, ANFP, coding sequence.
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Pred. No. 2.4e-09;
0; Mismatches 233;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Guegler KJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 and vesicle-trafficking disorders
                    BP.
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                  AAZ49052 standard; DNA; 1288
                                                                                                                                                                                                                                                                                                                                                                                                                                                        98US-0172977.
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                                                                                                (first entry)
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Matches 217; Conservative
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                                                                                                                                                                                                                                                                                                    diagnosis; ss
                                                                                                                                                                                                                                                                                                                                         Homo sapiens
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                                                                                                03-APR-2000
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                                                         AAZ49052;
AAZ49052
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Query Match
Best Local Similarity 48.2%;
Matches 217; Conservative
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                        649 agggggagctggaccagctgaaggagcatttgcggaaaggtgacaacctcgtcaacaagc 708
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                                                                                                                           aggateggetggaetgcacagecatgeattgggeetgcegeggggggeettagaggtgg
                                                           709 cagacgagcgcggcttcaccccctcatctgggcctccgcctttggagagattgagaccg
                                                                               tgaaacttctgcaaagccatggagcagacaccaatgtgagggataagctgctgagcaccc
                                                                                               769 ttogetteetgetggagtggggtgeegaeeeceacateetggeaaaagagegagageg
        tggaaggccacatggaaatcctggagaagcttctagataatggggccactgtggacttcc
                                                                                                                  cgctgcacgtggcagtccggacagggcaggtggagattgtggagcactttctatccctgg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "alternative splice site at position 604;
CAG trinucleotide at 605..607 results
from alternative splicing of exon 4"
                                                                                                                                                                                                                                                                                                                                                                     chromosome 19p12, immunosuppressive; immunomodulator; antinflammatory; antidiabetic; antiarthritic; gene therapy; inflammation; autoimmune diseases; transplant rejection; insulin dependent diabetes; multiple sclerosis; lupus erythematosus; rheumatoid arthritis; immunodeficiency; ss.
                                                                                                                                                                                                                                                                                                                                                              RFXANK; HSRFXANK; human; transcription factor; MHC class II;
                                                                                                                                                                                                                                                                                                                                              Human MHC class II gene transcription factor RFXANK cDNA
                                                                                                                                                                                                                                   1009 ccgactctggctacaccccgatggaccttg 1038
                                                                                                                                                                                                                           855 acctggcaggaaagaccccgacggacctgg 884
                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                        AAZ94868 standard; cDNA; 1345 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /number= 1
269..409
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755..855
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Novel isolated transcription factor, RFXANK, useful for treating MHC class II deficiency and autoimmune disorders, e.g. insulin dependent diabetes and multiple sclerosis, restores the functional transcription
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       than MHC class II genes, its inhibitors are devoid of other undesirable inhibitory effects.
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Score 77.2; DB 21; Pred. No. 2.4e-09; 0; Mismatches 233;

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Query Match
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                                                agggggagctggaccagctgaaggagcatttgcggaaaggtgacaacctcgtcaacaagc
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                            tggaaggccacatggaaatcctggagagcttctagataatggggccactgtggacttcc
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Viney EM, Willson TA;
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Nicola NA, Richardson RT,
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signalling protein (SOCS). SOCS can be used to screen for naturally occurring antibodies to SOCS, which may occur, e.g. in some autoimmu diseases. Alternatively, specific antibodies can be used to screen for SOCS, which is useful as a knowledge of SOCS levels may be important for the diagnosis of certain cancers. Soluble SOCS polypeptides can be used to treat disease, injury or abnormality involving cytokine mediated cellular responsiveness, e.g. hyperimmunity, immunosuppression, allergies and hypertension.
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                                                                                                                                                                                                                                                   Sequence 2649 BP; 559 A; 791 C; 749 G; 550 T; 0 other;
                                                                                                                                                                                                                                                                                                                                    Score 77.2; DB 19;
Pred. No. 2.9e-09;
0; Mismatches 228;
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Query Match 6.5%; Score 75.6; DB 22; Length 3454; Best Local Similarity 47.5%; Pred. No. 7.7e-09; Matches 225; Conservative 0; Mismatches 249; Indels 0;
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Db Qy 1413 gctacatctcagtagtggacaccctgaagatagtgaccgaagaaaccatgacca 1466

Search completed: April 17, 2002, 09:31:29 Job time: 4933 sec AJ34637 SHr-00001 AJ346193 SHr-00001 AJ346514 SHr-00001

F28615 HSPD17872 H F28533 HSPD17696 H F24152 HSPD10215 H F19619 HSPD04224 H AW237359 xm70f06.x

Perfect score:

Sequence:

OM nucleic

Run on:

Scoring table:

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Database

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Homo sapiens

Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

I (bases 1 to 749)

S NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

AL Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: Gapbs-refmail.nih.gov/.

Tissue Procurement: CLONETECH Laboratories, Inc.

CDNA Library Preparation: CLONETECH Laboratories, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov o column: 13

High quality sequence stop: 649.
          AJ346604 SHr-00001
BF775625 285833 MA
AA180314 Zp34902.s
F25326 HSPD12307 H
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AJ346346
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AW044467 wx22c10.x
B1413513 602987535
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BF19893 235854 MA
F32675 HSPD25601 H
F36591 HSPD3581 H
AJ346444 SHr-00001
BF189892 235852 MA
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8024.254 Million cell updates/sec
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1 cagctcgagggacggcacca......ctaccacaataaaaagctg 1158
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           GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                 11351937 seqs, 5372889281 residues
                                                                                                                                                                                                                       otal number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUMMARIES
                                                                                                                                                                                                                                                                             Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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BE926721
AJ346356
                                                      - nucleic search, using sw model
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Maximum DB seq length: 2000000000
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AJ346414 BF189892

399.2 393.6

415 410.2

Score

Result Š. 568.4 548.6 530.2 492.4 433.4 423.8

AJ346566 SHr-00001 AJ346339 SHr-00001

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. I (bases 1 to 610) NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap. National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

Tumor Gene Index Unpublished (1997)

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REFERENCE
AUTHORS
TITLE
                                                                                 JOURNAL
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                                                   5'-ATTCTAGAGGCCGAGGCGCCCATG-dT(30)BN-3' (where B = A, C, Or G and N = A, C, G, Or T). Average insert size 1.55 kb (range 1.0-4.0 kb). 15/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA).
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(Clontech); Site_1: Sfil (ggccgcctcggcc); Site_2: Sfil (ggccattatggcc); 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CACGCCATTATGGCC-3' and 3' adaptor sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  09-MAR-2000
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Pred. No. 2.1e-117;
0; Mismatches 12; Indels 5;
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Homo sapiens

ORGANISM

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/note="Organ: Kidney; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: ECO RI; Plasmid DNA from the normalized library NCI_CGAP_Kid3 was prepared, and ss circles were made in vitro. Pollowing HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneIDs 1322376-1333911, 1456007-1456775, and 1506552-1502855). Subtraction by Bento Soares and M. . . Fatima Bonaldo. "
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1;
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llarity 99.1%; Pred. No. 5.6e-113;
Conservative 0; Mismatches 4;
                                                                                                                                                                                            www-bio.llni.gov/bbrp/image/image.html
Insert Length: 691 Std Error: 0.00
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/clone_lib="NCI_CGAP_Kid11"
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High quality sequence stop: 462.
Location/Qualifiers
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Nit-MGC http://mgc.nci.nih.gov/.

Nit-MGC http://mgc.nci.nih.gov/.

Nit-MGC http://mgc.nci.nih.gov/.

Nit-MGC http://mgc.nci.nih.gov/.

Lonact: Robert Strausberg, Ph.D.

Email: capabb-:remail.nih.gov

Tissue Procurement: Gilbert Smith, Ph.D.

CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima

Bonaldo, Ph.D.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)

DNA Sequencing by:Incyte Genomics, Inc.

Clone distribution: NCI-CGAP Clone distribution information can be
found through the I.M.A.G.E. Consortium/LINL at:

http://image.llnl.gov

Plate: LLAM11354 row: e column: 09

High quality sequence stor: 31.

Location/Qualifiers

Ince /organism="Mus musculus"

/strain="Coation/Qualifiers"
/clone="Image: Taxon: 10090"

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602987535F1 NCI_CGAP_Lu33 Mus musculus CDNA clone IMAGE:5143664 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                   house mouse.
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
gogtgececageceagecagetacecagecectetgtgtgeageeggagggteetaag 1071
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                                        155 GCGTGCCCCAGCCCAGCTACCCAGCCCCTCTCTGTGTGCAGCCGGAGGGTCCTAAG
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                                                                                                                                                                 ccacaaactaccacaataaaaaagctg 1158
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Homo sapiens
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (Dases I to 504)
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagali, M.A., de Silvay, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,
Ragali, M.A., Ad Silvay, M. Jr., Zago, M.A., Bordin, S., Costa, F.F.,
Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare
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                                     69 GACATGCTAGTGCTAGAGGAAGAGCGCCTCGGGGTTCAGAGTCCTGCTTTACAAAAG
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/db_xref="taxon:9606"
/db_xref="bar0634"
/clone_lib="Bar0634"
/dev_stage="Adult"
/note="Organ: breast; Vector: pucl8; Site_1: Smal; Site_2: Smal; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196; 716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low
                                                                                                                                                      Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=QV2-BT0634-280
800-331-bl2&t3=2000-08-28&t4=1)
Seq primer: puc 18 forward
High quality sequence stop: 504.
1. 504
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                                                                                                               Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                              expressed
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 de Souza, S.J. and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 504;
                            human transcriptome with ORF
                                                Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
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,M.J., Soares,F., Brentani,R.R., Reis,L.F.,
Simpson,A.J.
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Pred. No. 2.2e-100;
0; Mismatches 1;
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                                                                                  Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
                           Shotgun sequencing of the
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//issue_type="pectoral muscle (after mastectomy)"
//issue_type="pectoral muscle (after mastectomy)"
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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University of Padua
Via U. Bassi 58/B, 35121 Padua, Italy
sequencing centre identifier: HSPD50428
ABI Chromatograms and other information are available on WWW
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Laveder, P., De Pitta, C., Toppo, S., Valle, G. and Lanfranchi, G. Specific subtraction of abundant mRNAs in skeletal muscle (Unpublished (2001)
Contact: Laveder P
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                                                                                                         AJ346356 456 bp mRNA ES:
SHr-000016-0-121 HM3/S3 Homo sapiens cDNA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 433.4; DB 10
Pred. No. 3.6e-87;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                           http://muscle.cribi.unipd.it
Seq primer: PC2R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone_lib="HM3/S3"
                                                                                                                                                              AJ346356.1 GI:15167539
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /sex="female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 37.4%;
Best Local Similarity 99.8%;
Matches 434; Conservative
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CCCAGCCCTCTCT
                                                                                                                                           AJ346356
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                                                                                                                                                                                                      human.
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181 CAGGAAAGACCCCGACGGACCTGGTGCAGCTCTGGCAGGCTGATACCCGGCACGCCCTGG 240
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/clone_lib="MARC 2PIG"
/tissue_type="pooled"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FORWARD: AGGAAACAGCTATGACCAT
BACKWARD: GTTTTCCCAGTCACGACG
Plate: 59 row: G column: 21
Seq primer: ATTTAGGTGACACTATAG.
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                                                                                                                                                                                                       1101 gccttttttctgcat 1115
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                                                                                                                                                                                                                     Homo sapiens
bikaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 435)
                                                                                                                               F24585 435 bp mRNA EST 13-MAY-1999
HSPD11011 HM3 Homo sapiens CDNA clone s4000015H03, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                at
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      741 aaatcaatgccagagacagggaaggggatactgcctgcatgacgctgtgaggctcaacc 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 AAATCAATGCCAGAGACAGGGAAGGGGATACTGCCCTGCATGACGCTGTGAGGCTCAACC 120
361 AGCTAACTGAGGGCCCAGCCTTTTTTCTGCATGATCCAGGAGCACATACCACAACTACC 420
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ABI Chromatograms and other information are available on WWW
http://grup.bio.unipd.it.
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Pred. No. 5.1e-85;
0; Mismatches 7; Indels 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1. 435
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="s4000015H03"
/clone_lib="HM3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                  Contact: Valle G.
CRIBI Biotechnology Centre
University of Padua
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /sex="female"
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F24585.1 GI:4810211
                             1144 acaataaaaaagctg 1158
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                                          421 ACAATAAAAAGCTG 435
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pig.

Sus scrofa

Mammalia; Butheria; Cetartiodactyla; Suina; Suidae; Sus.

(pases 1 to 567)

Fahrenkrug, S.C., Freking, B.A., Rohrer, G.A., Smith, T.P.L., Casas, E., Stone, R.T., Heaton, M.P., Grosse, W.M., Bennett, G.A., Laegreid, W.W. and Keele, J.W.

Stone, R.T., Mand use of two pooled tissue normalized cDNA libraries for EST discovery in swine

Unpublished (2000)
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                                                                              1041 ccctctctgtgtgcagccggagggtcctaagaatggctcccggagctaactgagggccca 1100
02-NOV-2000
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235854 MARC 2PIG Sus scrofa cDNA 5', mRNA sequence.
BF189893
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Pred. No. 3.1e-84;
0; Mismatches 46; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
TPL: 402 762 4366
Fax: 402 762 4390
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Score 415; DB 11;
Pred. No. 4.8e-83;
0; Mismatches 2;
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/db_xref="taxon:9606"
/clone="sH4-000004-3/E07"
/clone_lib="HM3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   up.plo.unipd.it.
Location/Qualifiers
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                                                                                              35.8%;
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                                                                                                                         Conservative
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(5.biotin-AACCGGCTGAGCGGCGGTTTTTTTTTTTTTTT-3'). The
ds cDNA was sonicated and size-selected in the range
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases I to 417)
Lanfranchi, G., Muraro, T., Caldara, F., Pacchioni, B., Pallavicini, A., Pandolfo, D., Toppo, S., Trevisan, S., Scarso, S. and Valle, G. Identification of 4370 expressed sequence tags from a 3'-end-specific cDNA library of human skeletal muscle by DNA genome Res. 6 (1), 35-42 (1996)
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                                                                                                                                                                                                                                                                                                                                                                                                                                               F32675 417 bp mRNA EST 13-MAY-1999 HSPD25601 HM3 Homo sapiens cDNA clone s3000045A02, mRNA sequence. F32675 GI:4818301
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University of Padua
Via Trieste 75, 35121 Padua, Italy
ABI Chromatograms and other information are available on WWW at
http://grup.bio.unipd.it.
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          535
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/note="Vector: pcDNAII (Invitrogen); Site_1: BstXI;
Site_2: NotI; The library was constructed by G.
Lanfranch: This library is not subtracted nor normal
The first strand CDNA was primed with a biotinylated
                                               gggggccacttagaggtggtgataaacttctgcaaagccatggagcagacaccaatgtgagg
                                                                                                                                                                                                                   gagcactttctatccctgggcctggaaatcaatgccagagacagggaaggggatactgcc
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="$300045A02"
/clone=lb="HM3"
/sex="female"
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Lanfranchi, G., Muraco, T. Caldara, F., Pacchioni, B., Pallavicini, A.,
Pandolfo, D., Toppo, S., Trevisan, S., Scarso, S. and Valle, G.
Identification of 4370 expressed sequence tags from a
3'-end-specific cDNA library of human skeletal muscle by DNA
sequencing and filter hybridization
Genome Res. 6 (1), 35-42 (1996)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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University of Padua
Via Trieste 75, 35121 Padua, Italy
ABI Chromatograms and other information are available on WWW
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HSPD33981 HM3 Homo sapiens cDNA clone sH4-000004-3/E07, mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         241 GCTGATACCCGGCACGCCCTGGAGCATCCTGAGCCGGNGGCTGAGCATAACGGGCTGAG
350-550 bp. The 3' specific fragments were selectionstreptavidin coated magnetic beads, ligated to non-palindromic BaxIX adapters, NotI digested and directionally cloned into BstXI-NotI cut pcDNAII of 124 c 130 g 68 t
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 423)
Laveder,P., De Pitta,C., Toppo,S., Valle,G. and Lanfranchi,G. Specific subtraction of abundant mRNAs in skeletal muscle Contact: Laveder P CRIBI Biotechnology Centre
                          /organism="Homo sapiens"
/db_xref="taxon:9606"
/db_xref="taxon:9606"
/clone_lib="HM3/S3"
/sex=female"
/tissue_type="pectoral muscle (after mastectomy)"
/tissue_type="pectoral muscle (after mastectomy)"
/note="Vector: pOPD (custom): Site_l: EcoRI; Site_2: Not caucasian; Skeletal muscle cDNA was depleted of hundred most expressed mRNAs through an original two steps
subtractive procedure"
a 125 c 118 g 66 t
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                                                                                                                                                                                                                                                                                                7 CAGGGAAGGGGATACTGCCCTGCATGACGTGTGAGGCTCAACCGCTACAAATCATCAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         367 ATCCAGGAGCACATACCACAACTACCACAATAAAAAGCTG 408
                                                                                                                                                                                                                       Query Match 34.7%; Score 402; DB 10; Best Local Similarity 100.0%; Pred. No. 3.9e-80; Matches 402; Conservative 0; Mismatches 0;
   Location/Qualifiers
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AJ346414.1 GI:15167597
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Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            University of Padua Via U. Bassi 58/B, 35121 Padua, Italy Sequencing centre identifier: HSPD50393 ABI Chromatograms and other information are available on WWW at http://muscle.cribi.unipd.it
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1 (bases 1 to 408)

Laveder, P., De Pitta, C., Toppo, S., Valle, G. and Lanfranchi, G. Specific subtraction of abundant mRNAs in skeletal muscle Unpublished (2001)

Contact: Laveder P.

CRIBI Biotechnology Centre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sapiens cDNA, mRNA sequence
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                                                                                                                                                                                                                                                    DB 11; Length 457;
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Pred. No. 5.8e-82;
0; Mismatches 5; Indels
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Homo
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sHr-000016-0-H10 HM3/S3
AJ346328
AJ346328.1 GI:15167511
'sex="female"
                                                                                                                                                                                                                                                   35.4%;
                                                                                                                                                                                                                                                 Query Match 35.4
Best Local Similarity 98.8
Matches 412; Conservative
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="HM3/S3"
/sex="female"
/tissue_type="pectoral muscle (after mastectomy)"
/note="Vector: pOPD (Custom); Site_1: EcoRI; Site_2: NotI;
caucasian; Skeletal muscle cDNA was depleted of hundred
most expressed mRNAs through an original two steps
subtractive procedure"
a 125 c 120 g 72 t
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Single pass sequencing. Bases called and alt_trimmed with phred
v0.980904.e. vector identified by cross_match with the -minscore 18
and -minmatch 12 options.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fahrenkrug,S.C., Freking,B.A., Rohrer,G.A., Smith,T.P.L., Casas,E. Stone,R.T., Heaton,M.P., Grosse,W.M., Bennett,G.A., Laegreid,W.W. and Keele,J.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Design and use of two pooled tissue normalized cDNA libraries for EST discovery in swine Unpublished (2000)
Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO BOX 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
1 (bases 1 to 537)
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0
                                                                                                                                                                                                                  Length 423;
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235852 MARC 2PIG Sus scrofa cDNA 5', mRNA sequence.
BF189892
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Pred. No. 1.7e-79;
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                                                                                                                                                                                                                34.5%;
99.3%;
                                                                                                                                                                                                                                 Best Local Similarity 99.3
Matches 401; Conservative
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Sus scrofa
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Bos taurus
Eukaryota; Metazoa: Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
1 (bases 1 to 504)
Smith, T. P.L., Grosse, W. M., Freking, B.A., Roberts, A.J., Stone, R.T., Casas, E., Wray, J.E., White, J., Cho, J., Fahrenkrug, S.C., Bennett
G.L., Heaton, M.P., Laegreid, W.W., Rohrer, G. A., Chitko-McKown, C.G., Pertea, G., Holt, I., Karamycheva, S., Liang, F., Quackenbush, J. and
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                                                                                                                                                               /organism="Sus scrofa"
/db_xref="taxon:9823"
/clone_lib="MARC_2PIG"
/tissue_Lype="pooled"
/lab_host="DH10B"
/note="Vector: pCMV SPORT6; Site_1: Xbal; Site_2: Xho
Library made from pooled tissue from testis, ovary,
endometrium, hypothalamus, pituitary, and placenta."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 393.6; DB 1:
Pred. No. 3.1e-78;
0; Mismatches 44.
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PCR PRIMETS
FORMARD: AGGAACAGCTATGACCAT
BACKWARD: GTTTTCCCAGTCACGACG
Flate: 59 row: G column: 19
Seq primer: ATTTAGGTGACACTATAG.
                                                                                                                      Location/Qualifiers
1..537
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BE809163.1 GI:10240275
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Best Local Similarity 90.5%;
Matches 420; Conservative
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bovine cDNA
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Sequence evaluation of four pooled-tissue normalized tabbraries and construction of a gene index for cattle Genome Res. 11 (4), 626-630 (2001)
                                                                                                                                                                                                                                                                                                                          71; Indels
                                 Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
TTE1: 402 762 4360
Fax: 402 762 4390
                                                                                                                                                                                                                                                                                                        Score 390.4; DB ]
Pred. No. 1.6e-77;
); Mismatches 71
                                                                                                                                                                                                                                                             adrenal, and endometrium."
                                                                                                                                                                                 /organism="Bos taurus"
/db_xref="taxon:9913"
/clone_lib="MARC 2BOV"
/tissue_type="pooled"
/lab_host="DH10B"
                                                                                                                                                                 Location/Qualifiers
1..504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              tggaaggccacatggaaatcctgg 518
|||| ||||||||||| ||||| |
TGGAGGCCACATGGAGATCCTTG 504
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                                                                                                                                                                                                                                                                                                        33.7%;
85.9%;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.
El (bases I to 412)
El (and Lanfranchi, G. Toppo, S., Valle, G. and Lanfranchi, G. Specific subtraction of abundant mRNAs in skeletal muscle
I Unpublished (2001)
Contact: Laveder P
CRIBI Biotechnology Centre
University of Padua
Via U. Bassi 58/B, 35121 Padua, Italy
sequencing centre identifier: HSPD50806
ABI Chromatograms and other information are available on WWW at http://muscle.cribi.unipd.it
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//scare_type="pectoral muscle (after mastectomy)"
/tissue_type="pectoral muscle (after mastectomy)"
/note="Vector: pOPD (custom); Site_1: EoRN: Site_2: Not
caucasian: Skeletal muscle cDNA was depleted of hundred
most expressed mRNAs through an original two steps
subtractive procedure"

124 c 118 g 71 t lothers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    agccgggggctgagcataacgggctggagggcctaatgatagtgggcgagagacccctc 989
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Pred. No. 3.5e-76;
0; Mismatches 7; Indels 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ctgcatgatccaggagcacataccacaaactaccacaataaaaaagctg 1158
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
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                                                       AJ346604.1 GI:15167787
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 33.2%;
Best Local Similarity 97.8%;
Matches 400; Conservative
                                                                                                                                                              Homo sapiens
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Smith,T.P.L., Grosse,W.M., Freking,B.A., Roberts,A.J., Stone,R.T., Casas,E., Wray,J.E., White,J., Cho,J., Fahrenkrug,S.C., Bennett,G.L., Heaton,M.P., Laegrenid,W.W., Rohrer,G.A., Chitko-McKown,C.G., Pertea,G., Holt,I., Karamycheva,S., Liang,F., Quackenbush,J. and
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/lab_host="DH10B"
/note="Vector: pCMV SPORT6; Site_1: XbaI; Site_2: XhoI;
Library made from pooled tissue from marrow, alveolar
macrophage, ovary, fetal semitendonosus muscle, and fetal
longissimus muscle."
140 c 160 g 77 t.
                                                                                                                                                                  Bos taurus
Sukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos
                                                                                                                                                                                                                                                                                                                                                                  Sequence evaluation of four pooled-tissue normalized bovine cDNA libraries and construction of a gene index for cattle Genome Res. 11 (4), 626-630 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Single pass sequencing. Bases called and alt_trimmed with phred v0.980904.e. Vector identified by cross_match with the -minscore and -minmatch 12 options.

PCR PRIMERS
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                                          BF775625 489 bp mRNA EST 285833 MARC 3BOV Bos taurus cDNA 5', mRNA seguence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
TTE1: 402 762 4366
Fax: 402 762 4390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 383.2; DB 11;
Pred. No. 6.6e-76;
0; Mismatches 58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: smith@email.marc.usda.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /db_xref="taxon:9913"
/clone_lib="MARC 3BOV"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FORWARD: AGGAAACAGCTATGACCAT
BACKWARD: GTTATCCCAGTACAGGACG
Plate: 87 row: K column: 20
Seq primer: ATTAAGGTGACACTATAG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Bos taurus"
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BF775625.1 GI:12123525
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87.8%;
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Matches 418; Conservative
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